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98US-0109869

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(INCY-) INCYTE PHARM INC
                             WPI; 2000-072605/06.
                                  N-PSDB; AAZ56761
               Lal
24-NOV-1998;
                  Bandman O,
Au-Young J;
                                                    disorders -
                                         Proteins,
              Tang YT',
SSSSXS
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Claim 1; Page 163; 229pp; English.

129 AA; Sequence

; Length 129; Indels 0; Mismatches , op

61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 61 δy

peripheral atherosclerosis.

/note= "Signal peptide" 28..129 /note= "Mature human TWEAKR protein"

AA256698 to AA256776 encode AAY57877 to AAX5955 which represent human transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiprollferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN. diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative polynucleotides, vectors, host cells and antibodies used Guegler KJ, Corley NC; Kaser MR, Baughn MR; 11 P, Hillman JL, Yue H, Patterson C, Gorgone GA,

Gaps 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 Score 571; DB 21; Pred. No. 1.8e-52; 93.98; 94.78; Query Match 93.9 Best Local Similarity 94.7 Matches 107; Conservative

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AAU03498 standard; Protein; 129 AAU03498

(first entry) 26-SEP-2001 AAU03498;

Human TWEAK receptor (TWEAKR) polypeptide.

TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; anglogenesis; coular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uvalits; macular degeneration; arthritis; rheumatism; malignant tumour; sarcoma, carcinoma; bengm tumour; haemophilic joint; preneoplastic condition; myocardial anglogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis;

Location/Qualifiers Homo sapiens Peptide Protein

Modulating anglogenesis in a manmal for treating diseases mediated by anglogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK 1..78 /note= "Extracellular domain" 79..101 /note= "Transmembrane domain" "Intracellular domain" 20-DEC-1999; 99US-0172878. 10-MAY-2000; 2000US-0203347 19-DEC-2000; 2000WO-US34755 102..129 /note= (IMMV) IMMUNEX CORP WPI; 2001-417975/44. N-PSDB; AAS03963 WO200145730-A2 28-JUN-2001 Wiley SR; receptor Domain Domain Domain

The sequence represents the human TWEAK receptor (TWEAKR) protein. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of annoiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopaths of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carchomas, malignant and metastatic conditions such as sarcomas and carchomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma; vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.

Example 1; Fig 1; 46pp; English.

129 AA; Seguence

Gaps Length 129; Indels . 6 93.9%; Score 571; DB 22; 94.7%; Pred. No. 1.8e-52; 0; Mismatches Matches 107; Conservative Similarity Query Match Best Local 9

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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 qq ò ò

AAU03500 standard; Protein; 309 AA 26-SEP-2001 (first entry) AAU03500; 61 AAU03500 RESULT XEXEXEX

Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.

Human normal ovari C glutamicum prote Human NAIL protein Human EST encoded

prostate tum

Human

Amino acid sequenc

AAY58207 AAM24485 AAY29189 AAY73883 AAX73883

Human EST encoded Human NPC1 (Nieman Human ORFX ORF2747

AAY43138 AAM23942 AAW88445

Title:

AAW23718 AAW22608

AAW81597

AAB42983

AAM41162 AAM42035

Protein encoded by Fragment HGJ1789 o Human polypeptide Human polypeptide Human transmembran

Platenolide syntha Platenolide syntha

Canine mature Flt-Canine Flt-3 ligan Human EST encoded

Smooth muscle prol

Smooth muscle prol Full length mouse Amino acid sequenc Human PRO1 protein

AAY13941 AAB73498 AAM39376 AAY56752 AAY56752 AAY64361 AAB70531 AAB70531 AAB70531 AAB70630

Human TANGO 215 pr Membrane-bound pro Human secreted pro Human PRO1344. Ho

Human transferase Human polypeptide Amino acid sequenc

PRO2 protein PRO1344 (UNO protein sequ

Human

ALIGNMENTS

AAB65218 AAB93670 AAB87544 AAB70532

AAU00401

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Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia, hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AlbS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein encoded by Gene No. 13.
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30-MAY-1997;
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AAW73409
 (without alignments)
354.656 Million cell updates/sec
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Human liver clone
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Human TWEAK recept
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                522463 segs, 74073290 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAW88506
AAV57940
AAU03498
AAU03500
AAY91463
AAY91604
AAY91552
AAY91552
AAR90537
AAR906337
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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Result ٠ ي

97US-0050935. 97US-0056250. 97US-0056293.

30-MAY-1997; 29-AUG-1997; 29-AUG-1997; HUMA-) HUMAN GENOME SCI INC

Dillon PJ, End Ruben SM, Yu G;

Rosen CA,

Carter

WPI; 1999-070209/06.

N-PSDB; AAV08823.

disorders or blood disorders

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This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAV84359-76) coding for 18 transmembrane proteins (see AAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as pen the cDNA. The host cells are used for the detection of ingands corresponding to the expressed proteins, and the screening of low mol. wt. medicines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder; reproductive disorder; smooth muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                          New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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Pred. No. 1.8e-52;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 152-153; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human transmembrane protein HTMPN-64.
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                                            (PROT-) PROTEGENE INC.
(SAGA ) SAGAMI CHEM RES CENTRE.
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94.7%;
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98US-0091674.
98US-0102954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.9 Best Local Similarity 94.7 Matches 107; Conservative
                                                                                                                                                         WPI; 1999-045730/04.
N-PSDB; AAV84374.
                                                                                                               Kato S, Sekine S,
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03-JUN-1997;
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02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
  Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The DNA sequences of the invention and their corresponding secreted
The DNA sequences of the invention and their corresponding secreted
The DNA sequences of the invention of treatment of the paper long sear useful for preventing, treatment or ameliorating medical
Conditions, e.g. by protein or gene therapy. Also pathological conditions
CC sample or by determining the presence of mutations in the DNA sequences.
CC Specific uses are described for each of the DNA sequences and the encoded
CC proteins, based on which tissues they are most highly expressed in, and
CC include developing products for the diagnosis or treatment of cancer,
Ctumours, neurological disorders, developmental abnormalities and foetal
deficiencies, blood disorders, leukaemias, diseases of the immune system
(including allergies or asthma), hepatic disease, Alzheimer's and
CC cognitive disorders, schizophrenia, prostate diseases, autoimmune
CC disorders and ALDS. The polypeptides are also useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                 New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and expressed in keratinocytes and to a lesser extent in endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 sdfclgcaaappapfrllwpilggalsltfvlgllsgflvwrrcrerssppp 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 607; DB 20; Length 114; 100.0%; Pred. No. 2.6e-56; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human liver clone HP10432-encoded membrane protein.
                                                                                                                                    Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane protein; HP10432; human; liver.
                                                                                                                                    Feng P,
                                                                                                                                 Endress GA,
                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 153; 188pp; English.
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Query Match
Best Local Similarity 100.4
Matches 113; Conservative

à g à

114 AA;

Seguence

98WO-JP02445.

03-JUN-1998;

12.

(first entry)

30-MAR-1999

AAW88506;

AAW88506

RESULT

Homo sapiens.

WO9855508-A2

10-DEC-1998.

17:1

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Gaps

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4

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Wiley SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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                                                 Domain
  Domain
                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU03500
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                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis; ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinopathy of prematurity; retrolental fibroplasia; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischemenia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis;
                                                                                                                                                                                                                               transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN.
                                                                                                                                                                                                                     AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
                                                                                                                                 Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guegler KJ, Corley NC;
Kaser MR, Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                             Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Signal peptide"
28..129
/note= "Mature human TWEAKR protein"
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                                                                                                                                                                                                                                                                                                                                                                                              Score 571; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.8e-52;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TWEAK receptor (TWEAKR) polypeptide.
                                               JL, Yue H,
Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU03498 standard; Protein; 129 AA.
                                                                                                                                                                                             Claim 1; Page 163; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             93.9%;
94.7%;
98US-0109869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral atherosclerosis
                                              al P, Hillman
Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                         (INCY-) INCYTE PHARM INC
                                                                                               WPI; 2000-072605/06.
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                         129 AA;
                                                                                                           N-PSDB; AA256761
                                                 La]
24-NOV-1998;
                                              Tang YT, La
Bandman O,
Au-Young J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 107;
                                                                                                                                                                         disorders -
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU03498;
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angiogenesis, to be used in the treatment and diagnosis of human disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the human TWEAK receptor (TWEAKR) protein. The TWEAK protein is a member of the tumour necrosis factor (TWF) family an induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benign tumours and preneoplastic conditions, myocardial anglogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 571; DB 22; Length 129;
Pred. No. 1.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                             79.101
/note= "Transmembrane domain"
102.129
/note= "Intracellular domain"
1..78 /note= "Extracellular domain"
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000; 2000WO-US34755
                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0172878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2000; 2000US-0203347
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Best Local Similarity 94.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-417975/44.
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                                                                                                                                                                                                                                    WO200145730-A2.
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The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKR) protein extracellular domain fused to an Fc portion from human iggl. This fusion protein, TWEAKR-Fc, is used in the preparation of TWEAKR agonists and antagonists. The TWEAK protein is a majogenesis. TWEAKR may therefore be used to screen for and develop angiogenesis. TWEAKR may therefore be used to screen for and develop tweak angiogenesis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular mediated by angiogenesis include ocular disorders characterised by ocular mediated by angiogenesis include ocular disorders characterised by ocular mediated by angiogenesis include ocular disorders characterised by ocular rectinoplastoma, retinopathy of prematurity, retrolental fibroplasia, retinoplastoma, retinopathy of prematurity, retrolental fibroplasia, retinoplaston, and inflammatory diseases such as arthritis, removascularisation, and inflammatory diseases such as arthritis, remematism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and metastatic conditions such as sarcomas and carcinomas, benign tumours and scleroderma, vascular adhesions, atherosclerosis, hemophilic joints, scleroderma, vascular adhesions, atherosclerosis, peripheral atherosclerosis and ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK
TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis; ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinobastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; human IgG1; TWEAKR-FC; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "From TWEAKR extracellular domain. Specifically referred to in Claims 4 and 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Mature human TWEAKR-Fc fusion protein.
Specifically referred to in Claim 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "From a BglII cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 45-46; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000; 2000WO-US34755
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2000US-0203347
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N-PSDB; AAS03965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
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10-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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309 AA;

Sequence

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1;
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                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiarthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16:
                                     Gaps
                                                                                         1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encode,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Υ;
                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                   22;
                                                                                                                                         61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                             Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moore PA,
PE, Brewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucenski M;
                                     Indels
 Score 433; DB 22;
Pred. No. 1.3e-37;
2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Komatsoulis GA, Rosen CA, Ruben SM, Duan R
Lafleur D, Wei Y, Ni J, Florence KA, Youn
Soppet DR, Endress GA, Ebner R, Olsen HS,
                                     2; Mismatches
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                                                                                                                                                                                                                                                               AAY91463 standard; Protein; 112 AA.
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98US-0095486.
98US-0095454.
98US-0095455.
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   71.28;
74.18;
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-195282/17.
N-PSDB; AAA26358.
                     Similarity
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                                       83;
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                                                                                                                                                                                                                                                                                                 AAY91463;
     Query Match
Best Local S
                   Best Loca
Matches
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cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners.

AAAA26337 to AAA26345 and AAY91450 are sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein sequence encoded by gene 13 SEQ ID NO:277.
                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                           DB 21; Length 112;
                                                                                                                                                                                                                                                                                                                                           MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC
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ig PE, Brewer I
Mucenski M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed in. Examples of the activities are: cytostatic;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                               1.9e-21;
0;
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Y, Ni J, Florence KA, Young
ess GA, Ebner R, Olsen HS, M
                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                           Score 274.5;
                                                                                                                                                                                            exemplification of the present invention.
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98US-0095454.
98US-0095455.
                                                                                                                                                                                                                                                                           45.18;
96.48;
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Endress GA, E
                                                                                                                                                                                                                                                                                                            Conservative
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Lafleur D, Wei Y,
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                           112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY91604;
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antiallergic; osteopathic; antiantinitian and controlled antial antidiabetic; antial experience antial experience. The corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions and be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, developmental abnormalities and foetal deficiencies, blood disorders, developmental abnormalities are alternated and metabolic disorders, schizophrenia, osteoporosis, arthritis, infections, Alls, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psortasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also useful for identifying their binding partners.

AMALGIST to AMALGIST on AMALGIST are sequences used in the
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  immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human.secreted protein sequence encoded by gene 13 SEQ ID NO:225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ebner R, Olsen HS, Mucenski M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 274.5; DB 21;
Pred. No. 2.7e-21;
---rhes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
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Lafleur D, Wei Y, Ni J, Florence KA,
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98US-0095454.
98US-0095455.
98US-0096319.
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96.4%;
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Endress GA, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
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Best Local Similarity
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N-PSDB; AAA26447

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/note= "claimed"
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                                                                          Purified or
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                                                                                                                                                                                                                                                            Appressor in. Examples of the activities are: Cytostatic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins. Dased on which tissues they are most highly expressed in, and include developing products for the disquoses of the immune system, and foretal deficiencies, blood disorders, developmental abnormalities and foretal diseases, inflammation, allergies, Alzheimer's and behavioural diseases, inflammation, allergies, arthritis, infections, AIDS, spinal cord injuries, cardiovascular disorders, asthma, sepsis, acne, psoriasis, cardiovascular disorders asthma, sepsis, acne, psoriasis, cardiovascular disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners.

AAA26337 to AAA26345 and AAA26345 are sequences used in the exemplification of the present invention.
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                                                                                                                                                                    The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UL144; death receptor; apoptosis; programmed cell death; FAS;
TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptides they encouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF receptor apoptosis mediated protein (TRAMP) death receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 274.5; DB 21; Length 156;
Pred. No. 2.7e-21;
1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC
                                                                                                                                                                                                                                                  expressed in. Examples of the activities are: cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                      Claim 11; Page 528; 634pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200034335-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature UL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related
urified or recombinant polypeptide for modulating apoptosis comprises sequence which binds to an antibody specific for UL144 or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------degtelpgfyehg 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 DFCLGCAAAPPAPFRLLW-----PILGGALSLTFVLGLLSGFLV-----W 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA--RPHS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2810 anti-Mullerian hormone receptor; anti-Mullerian hormone; AMH; receptor; antibody; therapy; H1; 2810; tumour; transforming growth factor-beta; TGF-beta; bone morphogenic protein; activin; Mullerian inhibiting substance; MIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 80.5; DB 21; Length 426; 22.2%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "signal peptide"
                                                                                                                              Disclosure; Page 64-65; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR80631 standard; Protein; 508 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 RRC------RRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 rhcwphkplvtadeagmealtppp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 22.2 32; Conservative
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Homo sapiens.
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8
                                                                                                                                                                                                                                                                                                                                                               structurally and functionally related to TGF-beta bone morphogenic protein, and activin. AMH receptors are present in a limited number of tissues and can therefore be used to design antibody-toxin complexes to target tumour cells in these tissues. The AMH-receptor sequences can be used to screen and purify compounds that bind to them, thereby identifying AMH ligands. The antibody designed from the receptor sequences can be used in immunoassays to detect the levels of AMH-receptor. The antibody can also be linked to a toxin in order to kill cells that express the receptor, e.g. cancer cells. The advantage of using antibody conjugates based on AMH-receptors are that they can be used more aggressively than those based on antibodies that recognise
                                                                                                                                                                                                                                                                                                               This sequence represents the 2B10 anti-Mullerian hormone (AMH) receptor isoform. The difference between this isoform, and the H1 isoform (see AAR80632) is that H1 contains a extra exon. AMH is a glycoprotein and is part of the transforming growth factor beta superfamily. AMH is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 nanyshlpplggpgtpgpggpgaapgespwmalallglvlllllllggivvallgrkayr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 -----LGCAAAP-----PAPFRLLW---PILGGALSLTFVLGLLSGFLVWRRCRR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                polypeptide(s) and antibodies - useful in immunoassays screening for ligands, treatment of cancer cells expressing the receptor etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 LGLWLALLRSVAG---EQAPG----TAPCSRGSSWSADLDKCMDCASCRARPHSDFC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 lglwallpaavggcrdsdepgceslscdpsprarassgst-lftc----scga----dfc 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
13.2%; Score 80.5; DB 16; Length 508;
Best Local Similarity 31.5%; Pred. No. 2.1;
Matches 40; Conservative 9; Mismatches 41; Indels 37
                                                                                                                                                                                                                                  New DNA encoding anti-Mullerian hormone receptor, related
                                                                                                                            (BIOJ ) BIOGEN INC.
(INRM ) INSERM INST NAT SANTE & RECH MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:17233.
                                                                                                                                                                                                                                                                                     Claim 4; Page 45-46; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95174 standard; Protein; 224 AA.
                                                             94WO-US14643.
                                                                                       93US-0173512
                                                                                                   93US-0166333
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                                                                                                                                                                                           WPI; 1995-231521/30.
N-PSDB; AAQ98986.
                                                                                                                                                                   Josso N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ERSSPPP 113
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          WO9516709-A2
                                                             .3-DEC-1994;
                                                                                     23-DEC-1993;
                                                                                                    13-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                     22-JUN-1995
                                                                                                                                                                   Cate RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the polynucleotide which comprises a 1-end sequence, where the oppination of the comprises at least 15 nucleotides and the combination of the complementary to a polynucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAS. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the full-length cDNAS. The primers allow obtaining of the full-length cDNAS assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human cDNA sequences; AAB92446 to AAB95893 represent human anino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID 17233; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%; Score 79; DB 29.7%; Pred. No. 1.3; iive 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                  99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                         28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                            02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST
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EP1074617-A2
                                                                                                                                                                                                                                                                                       11-JAN-2000;
                                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                                                                                                                     27-AUG-1999;
                                                                      07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transuluminal coronary angioplasty (PTCA), or myoma, hematopoietic cell-
regulatory activity, cytokine activity, tissue generation/reparation
activity, actin/inhibitin activity, taxis and chemotaxis activity, blood
coagulation/thrombotic activity, receptor/ligand activity, cadohelin/
tumour metastasis inhibiting activity; tumor inhibition, and as nutrient.
The present sequence represents the protein of the invention which can be
used for modulating smooth muscle cell proliferation.
                                              Cell proliferation; vascular; smooth muscle cell; arteriosclerosis; PTCA; endothelial thickening; percutaneous transuluminal coronary angloplasty; myoma; hematopoietic cell-regulation; cytokine; tissue generation; taxis; actin activity; chemotaxis; blood coagulation; thrombotic; tumor; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                The invention provides mouse polypeptides for treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be produced by standard recombinant methodology. The polypeptides can be used according to their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or renarrowing by vascular endothelial thickening after percutaneous
                                                                                                                                                                                                                                                                                                                                      Novel mouse polypeptides for treatment, e.g. arteriosclerosis and myoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRARPHSDF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 lkriltvtilalwl-----phpgnaqqqctngfdldrqsgqcldidecrtipea-- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A55 protein; mouse; smooth muscle proliferation; tissue generation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 crgdmmcvnqnggylciprtnpvyrgpysnpystsysgpypaaappvp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLG------AAAPPAP 74
                       Smooth muscle proliferation modulating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 77; DB 2
Pred. No. 4.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Full length mouse A55 protein seguence.
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 42-44; 70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                         Tashiro K, Nakamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY54990 standard; Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.7%;
Best Local Similarity 24.1%;
Matches 26; Conservative
                                                                                                                                                                                              99WO-JP02283
                                                                                                                                                                                                                        98JP-0119731
                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ39383, AAZ39384.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                  (ONOY ) ONO PHARM CO LID.
                                                                                                 metastasis; nutrient.
                                                                                                                                                                                                                                                                                                WPI; 2000-038646/03
                                                                                                                         Mus musculus.
                                                                                                                                                                                                28-APR-1999;
                                                                                                                                                                                                                        28-APR-1998;
                                                                                                                                               WO9955863-A1
22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2000
                                                                                                                                                                       04-NOV-1999
                                                                                                                                                                                                                                                                          Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY54990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY54990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
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human ASS protein. The protein can be used for the treatment of diseases due to abnormal proliferation of smooth muscle. The polypeptides can be used according their inhibition of the proliferation of vascular smooth muscle cells, particularly in treating arteriosclerosis or re-narrowing by vascular endothelial thickening after percutaneous transluminal coronary angioplasty (PTCA), or myoma, haematopoietic cell-regulatory activity, cytokine activity, tissue generation/reparation activity, activity, taxis and chemotaxis activity, blood coagulation/thrombotic activity, receptor/ligand activity, coagulation/thrombotic activity, receptor/ligand activity, cadherin/tumour metastasis inhibiting activity; tumour inhibition, and as
vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma; vascular endothelial thickening; haematopoletic cell-regulator; cytokine; percutaneous transluminal coronary angioplasty; blood coagulation; PTCA, actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides for treatment of, e.g. arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRARPHSDF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence is the mouse A55 protein. The invention relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoregulation; tumour; cancer; autoimmune disease; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 77; DB 21; Length 448; 24.1%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crgdmmcvnqnggylciprtnpvyrgpysnpystsysgpypaaappvp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- AAAPPAP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine mature Flt-3 ligand splice variant clone 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 52-55; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY58208 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CLG------C------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura
                                                                                                                                                                                                                                                                                                                                                               99WO-JP02284.
                                                                                                                         tumour metastasis inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-0119731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ONOY ) ONO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Honjo T, Tashiro K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-038647/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ40029
                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09961618-A2
                                                                                                                                                                                                                                                                                                                                                                   28-APR-1999;
                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                               WO9955864-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2000
                                                                                                                                                                                                                                                                                                       04-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY58208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
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Yang S, Dreitz MJ, Wonderling RS;

Sim G,

(HESK-) HESKA CORP.

29-MAY-1998; 28-MAY-1999; 02-DEC-1999

2000-072623/06

99WO-US11942. 98us-0087306

Canis familiaris. WO9961618-A2.

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5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligand. The invention relater to canine interleukin-4 (II-4), canine or feline CD154 (CD40 ligand), canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GMCSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 rlvlagrwmvrlgavagsgmgilleavnteihfvtfcafgdtsgglaalkpwitrrnfsg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 DLD-KCMDCASCRARPHSDFCLGCAA--APPAPFRLLWPILGGALSLTFVLGLLSGFLVW 101
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAY58204 and AAY58206-Y58209 respectively represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
                                                                                                                                                                                                                                                   Wonderling RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine Flt-3 ligand splice variant clone 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.6%; Score 76.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3b; Page 177-178; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58207 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection, and in drug targetting.
                                                            99WO-US11942.
                                                                                                                                                                                                                                                   Yang S, Dreitz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.5%;
                                                                                                                         98US-0087306
                                                                                                                                                                                                                                                                                                         WPI; 2000-072623/06.
N-PSDB; AAZ55507, AAZ55508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 27.5
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 RRCRRERSSPP 112
                                                                                                                                                                                      (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AA;
                                                            28-MAY-1999;
                                                                                                                      29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000
02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                   Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
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Sequences AAY58204 and AAY58206-Y58209 respectively represent encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while sequences AAY58210-Y58211 represent encoded and mature felline Flt-3 ligand. The invention relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand, canine or feline CD40, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline interferon-alpha (FRV-alpha) and feline granulocyte macrophage colony-stimulating factor (GMCF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including alleries, inflammantion and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense in alleries). The proteins may be used in cathing and to a protein or alleries encoundation or an alleries and to a protein or alleries and to a screen for modulatory therapeutics (e.g., antisense in alleries). The proteins may be used in a protein or and a protein or a prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 DLD-KCMDCASCRARPHSDFCLGCAA--APPAPFRLLWPILGGALSLTFVLGLLSGFLVW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- EQAPGTAPCSRGSSWSA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.6%; Score 76.5; DB 21; Best Local Similarity 27.5%; Pred. No. 2.9; Matches 36; Conservative 15; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ55503, AAZ55504, AAZ55505, AAZ55506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3b; Page 172-173; 264pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection, and in drug targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RLLVLGLWLALLRSVAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rrrrrrspyp 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
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Search completed: March 12, 2002, 09:56:32

Job time: 89 sec

Flt-3 ligand; antibody; canine; feline; inhibitor; immune response; immunoregulation; tumour; cancer; autoimmune disease; vaccine.

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748.431 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_vertebrate:*

sp_organelle:*

sp_phage:*

sp_plant:* sp_rodent:* sp_virus:*

	Description	Q9np84 homo sapien	O9qzw3 mus musculu			Q9bzq3 homo sapien	ОШО		OMO	Q9nOb3 macaca fasc	Q42839 hordeum vul	Q9qee6 indian citr	O53668 mycobacteri	018288 caenorhabdi	Q9h460 homo sapien	Q9a9x4 caulobacter	P90890 caenorhabdi	Q9p2p7 homo sapien	004393 hordeum vul	Q98th8 cyprinus ca
SUMMARIES	ID	Q9NP84	Q9QZW3	Q9CR75	Q9HCS0	Q9BZG3	Q9BZG2	014866	014865	Q9N0B3	042839	Q9QEE6	053668	018288	09н460	Q9A9X4	P90890	Q9P2P7	004393	098тн8
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Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W., Testa J.R., Peifley K.A., Winkles J.A.; "The Fn14 immediate-early response gene is induced during liver regeneration and highly expressed in both human and murine

SEQUENCE FROM N.A. TISSUE=PLACENTA; MEDLINE=20216634; PubMed=10751351;

SEQUENCE FROM N.A. Tanaka S., Sugimachi K.; "Human homologue of Fn14."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

NCBI_TaxID=9606;

hepatocellular carcinoma.";
Am. J. Pathol. 156:1253-1261(2000).
SEQUENCE FROM N.A.
TISSUE-ENDOMEFRIAL ADENOCARCINOMA;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
EMBL; AB035480; BAA94792.1;
EMBL; AR191148; AAR69108.1;
EMBL; BC002718; AAH02718.1;

POTENTIAL. BF3FDFB9C1E1C448 CRC64;

9 31 P

Signal, Transmembrane. SIGNAL 9 31 SEQUENCE 129 AA; 13

	20	72.	5	11.	0	329	4	Q9NQD2		Q9nqd2 homo sapien
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	30	70	5	•	9	412	7	Q9FCA1		Q9fcal streptomyce
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10	dN60	84		PRE	PRELIMINARY	IARY:		PRT:	129 AA.	
AC	09NP84;	84;								
DŢ	01-OCT-2000	CT-20	000	(Tr	TrEMBLrel		15,	Created)		
DŢ	01-0	01-OCT-2000	000	(Tr	TrEMBLrel.		15,	Last seq	sequence update)	
DŢ	01-JUN-2001	UN-20	001	(Tr	TrEMBLrel		17,	Last ann	annotation update)	
DE	TYPE	н	RANS	MEN	TRANSMENMBRANE	IE PR	OTEI	N PRECUR	PROTEIN PRECURSOR (TYPE I TRANS)	I TRANSMEMBRANE PROTEIN
DE	FN14).									
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OS	Ношо	sab	iens	H)	Homo sapiens (Human)					
႘	Enka	Eukaryota; Metazoa;	æ e	leta	zoa;	Chordata;	date			uteleostomi;
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SEQUENCE
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                       Gaps
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MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                    FGFRP2 OR FN14.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
MEDLINE-20020297; PubWed=10551889;
MEDLINE-20020297; PubWed=10551889;
Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.
Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins Richards C.M., Winkles J.A.;
Richards C.M., Winkles J.A.;
"The mitogen-inducible Fn14 gene encodes a type I transmembrane protein that modulates fibroblast adhesion and migration.";
J. Biol. Chem. 274:33156-33176(1999).
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                                                                                                    61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 450; DB 11; Length 129; 75.2%; Pred. No. 6.3e-38;
Length 129;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA; 13637 MW; 14B5C68EEF493385 CRC64;
                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TYPE I TRANSMEMBRANE PROTEIN FN14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FIBROBLAST GROWTH FACTOR REGULATED PROTEIN 2.
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Score 571; DB 4;
Pred. No. 4.5e-50;
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                      0; Mismatches
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                                                                                                                                                                       PRT;
93.98;
94.78;
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Matches 85; Conservative
                       Matches 107; Conservative
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          Similarity
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Q9CR75;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Saito R., Arakada K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rober D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakai K., Okido T., Fuult C., Fulthoff M., Batdarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ruonstein M.J., Hult D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ashing P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Savaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Whittaker C., Wilming L., Wanshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Manachia V., Vanachia V., Vanachia V., Vanachia V., Vanachia V., Vanachia V., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TYPE I TRANSMEMBRANE PROTEIN PRECURSOR.
FN14 VARIANT.
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Pred. No. 2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AK005530; BAB234101.1; ..
EMBL; AK005382; BAB23989.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 74.3
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
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m

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HSSP; P19438; INCF.
InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEATH RECEPTOR 3 BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P19438; 1NCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
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                                           014866
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RESULT
014866
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014865
                                                                  AC OCC OCC OCT DE TRAPER BY A DETTRAPER BY A DETTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yousef G.M., Diamandis M.E., Diamandis E.P.;
"Molecular cloning of the human hormonally regulated testicular acid phosphatase gene, and its down-regulation in testicular cancer.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR312918; AAK09396.1; --
SEQUENCE 333 AA, 35402 MW; 0C0237096567B30F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Yousef G.M., Diamandis B.P.;
Yousef G.M., Diamandis M.E., Diamandis E.P.;
Yousef G.M., Diamandis M.E., Diamandis E.P.;
Wolecular cloning of the human hormonally regulated testicular acid phosphatase gene, and its down-regulation in testicular cancer.";
Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A73121918; AAK093931.;
-EBMBL, A73121918, AAK093931.;
-EBMBL, A73121918, AAK093931.;
-EBMBL, A73121918, AAK093931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 PG-TAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGC--AAAPPAPFRLLWPILGGALS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 87; DB 4; Length 333;
Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 87; DB 4; Length 426; 35.3%; Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Indels
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                                                                                                           Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                333 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 LTFVLGLLSGFLVWR-RCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 VLVALSLGLGLLAWRPGCLRALGGP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 LIFVLGLLSGFLVWR-RCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 VLVALSLGLGLLAWRPGCLRALGGP 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
35.3%;
                                                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, ACID PHOSPHATASE VARIANT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
ACID PHOSPHATASE
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                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                         Homo sapiens (Human)
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                      Q9BZG3;
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                                                                09BZG3
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                      RESULT
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                                           O9BZG3
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145 GALHRHTRLL-------CSRRDT------DCGTCLPGFYEHG 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA--RPHS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salles G.;
"A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas.";
Biochem. Biophys. Res. Commun. 242:376-379(1998).
EMBL: AF026070; AAC39556.1;
                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Warzocha K., Ribeiro P., Renard N., Charlot C., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98113360; PubMed-9446802;
Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                      Salles G.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026071; AAB82288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D19F3E847BFC093 CRC64;
                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%; Score 85.5; DB 4; 26.2%; Pred. No. 0.45;
277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 1.
SEQUENCE 277 AA; 29111 MW; 3D19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                  SOLUBLE DEATH RECEPTOR 3 BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000561; EGF-like.
InterPro; IPR001368; TNFR_C6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 26.2%
Matches 32; Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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NCBI_TaxID=4513;
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Q42839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBOURING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                          145 GALHRHTRLL----------CSRRDT------DGGTCLPGFYEHG 173
                                                                                                                                                                                                                                                                                        62 DFCLGCAAAPPAPFRLLW------PILGGALSLTFVLGLLSGFLV------W 101
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  4 GSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA--RPHS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: TO THE EUKARYOTIC CONDEXIN FAMILY.
EMBL; AB046017; BAB01599.1; -.
InterPro; IPR000500; Connexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TO-2000 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
GAP JUNCTION PROTEIN (CONNEXIN).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SUBUNIT: A CONNEXON IS COMPOSED OF AN HEXAMER OF CONNEXINS
                                                                                                                                                                           13.2%; Score 80.5; DB 4; Length 426; 22.2%; Pred. No. 2.1; ive 13; Mismatches 34; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.0%; Score 79; DB 6; Length 341 Best Local Similarity 27.9%; Pred. No. 2.4; Matches 29; Conservative 9; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gap junction; Transmembrane.
SEQUENCE 341 AA; 36784 MW; 4A71DEA938F0FA0C CRC64;
                                                                                                                                  371AA7F16AD29C16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                341 AA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00006; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00565; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_1; 2.
PROSITE; PS60050; TNFR_NGFR_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                              102 RRC------RRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00407; CONNEXINS_1; 1. PROSITE; PS00408; CONNEXINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                            234 RHCWPHKPLVTADEAGMEALTPPP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
                                                                                                                                                                           Query Match 13.2%
Best Local Similarity 22.2%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9541;
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|------RPPCTGVVDCY 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aleurone-specific expression of a barley chitinase gene.";
Plant J. 6:579-589(1994).
-!- CATALYTE ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
EMBL; L34211; AAA56787.1;
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of an enhancer/silencer sequence directing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.9%; Score 78.5; DB 10; Length 332; 32.0%; Pred. No. 2.7; tive 9; Mismatches 38; Indels 23
                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4 BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B38554F49AC9E0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 CLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWR-RCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSGCGPTPPGPSP-----GGGVSSIISRDLFEQFLLHRDRCQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13. Created)
01-MAY-2000 (TrEMBLrel. 13. Last sequence update)
01-UNN-2001 (TrEMBLrel. 17. Last annotation update)
23 KDA PROTEIN.
                                                                             69 AAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP
                                                                                                              PROSITE; PS00773; CHITINASE 19_1; UNKNOWN_1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AA.
                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                     332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendel, 1565; Horvu; Chial; 1565.
InterPro; IPR001002; Chitin bind.
InterPro; IPR0010026; Clyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITTNBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000674; Glyco_hydro_19; 1.
ProDom; P0000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chitin-binding; Glycosidase; Hydrolase
                                                                                                                                                                                                                                                                     PRT;
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MEDLINE-95078949; PubMed-7987416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AA; 35369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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9 LIRLIVLGIMLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA 68

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348 AA; 37805 MW; 07EB6478067F8995 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ::| : |
149 WMTCLVGAIIG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 SLIFVLGLLSG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                             018288
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                                                                                                                                              RESULT 13
018288
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Q9H460
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Gas S., Barry C.E. III, Trekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Sqares Y., Sulston J.E.,
Taylor K., Whitchead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 ALPHR--IVPRVHAAPGLHKLVYVGWTAIRTNGWYRRYLLVQVLFGSVVLGSSFHSIRVA 259
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 MPSGTARARILLTEVGVGAALTAVVAATLSFVPDQHPLSRNIHLLWTAAVAMAISAAICR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RGSLRRLLRLLVLGLWLALLRSVAGEQAP-GTAPCSRGSSWSADLDKCMDCASCRA--RP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 RGSQIRSVRLLP---WRPFTRFPV---CPSGTSPYSRGTHSQPSYVRCQNCERARQWFRA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARGSLRRLLRLLVLGLWLALLRSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR 56
                                                                                                                                                                                      "Indian citrus ringspot virus: a proposed new species with some affinities to potex-, carla-, fovea- and allexiviruses."; submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF184962; AAF01314.1.; SEQUENCE 222 AA; 25455 MW; 636A47058DDBDDDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
12.4%; Score 75.5; DB 2; Length 436;
Best Local Similarity 23.0%; Pred. No. 6.7;
Matches 35; Conservative 16; Mismatches 52; Indels 49
                                                                                                                                           Rustici G., Accotto G.P., Noris E., Masenga V., Luisoni E.,
Milne R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA; 45325 MW; 393ABC2532F42D2A CRC64;
                   Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=104664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 HDGPRCLHQRPDYSRLQAPPDPFQHLNSFEPILLAALSV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 H-SDFCL-----GCAAAPPAPFRLL---WPILGGALSL 88
                                                                                                                                                                                                                                                                                                                                                             12.4%; Score 75.5; DE 35.4%; Pred. No. 3.8; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ARPHSDFCLGCAAAPPAPFRLLW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome sequence.";
Nature 393:37-544(1998).
EMBL; AL021929; CAA17338.1;
Tuberculist; RV0246;
Indian citrus ringspot virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN 1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2000 (TrEMBLrel. 14, PUTATIVE MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.49
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RV0246 OR MTV034.12
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                                                                                              SEQUENCE FROM N.A.
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SEQUENCE 436 AA;
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92 PTTAYKNGGLSF---LIAYVVCGILFAVPAIHMEFALGQYAAKSPPAAFRRMPILEGVG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 PGTAPCSRGSSWSADLDKCMDCASCRARP--HSDFCLG--CAAAPPAPFRLLWPILGGAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heath P.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: J1749; CAC10186.1; -
InterPro: IPR000500; Connexin.
Pfam: PF00029; Connexin: 1
PRINTS: PR00206; CONNEXIN.
SMART; SM0037; CNN; 1.
PROSITE; PS00407; CONNEXINS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gardner A., Mcmurray A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 281503; Asb04115.1; -.
EMBL; 282083; CAB04115.1; -.
EMBL; 282083; CAB04975.1; -.
EMBL; 281503; CAB04975.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 635 AA; 71267 MW; 2841834039D8F14A CRC64;
                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BA425A6.2 (SIMILAR TO CONNEXIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.4%; Score 75.5; DB Best Local Similarity 36.6%; Pred. No. 9.2; Matches 26; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AA.
                                                                                                                                                                                         635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000175; Na_neurotran_symport.
Pfam; PF00209; SNF; 2.
------ALSLTFVLGLLSGFLVWRRCR 105
                               1: | :| | | 260 AVPGDQPDEVVAVVLFVCVGLLGGIALWNRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00176; NANEUSMPORT.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, ZK1010.9 PROTEIN.
                                                                                                                                                                                           PRELIMINARY;
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MEDLINE-21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.E., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. SGI. US.A. 98:4136-4141(2001).
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                                                                                                                                                           9 LLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LLRLLVLGLWLALLRS-VAGEQAPGTAPCSRGS------SWSADLDKCMD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus.
Bacteris Proteobacteria; alpha subdivision; Caulobacter group; Caulobacter.
Caulobacter.
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    Score 75; DB 4; Length 348; Pred. No. 6.2; 9; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll protein; Complete proteome.
519 AA; 53934 MW; F37A3A52753DB53B CRC64;
                                                                                                                                                                                                                                                                                                                      69 AAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                                                                                                                                                                                                                       166 VSRPTEKSLLMLFLWAVSALSFLLGLADLVCSLRRRWRRPGPP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN CC0837.
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        12.3%;
27.9%;
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Best Local Similarity 24.3
Matches 33; Conservative
Query Match 12.3
Best Local Similarity 27.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Db 370 VSAEDTPDLLAISPTP 385 Search completed: March 12, 2002, 09:59:48 Job time: 195 sec

104 CRRERS-----SPPP 113

| | | | | | | | | | | 310 LVSRDAALLSQVLLRVLXMVPIAFVWVRGAESLPAWALAGPAAAVTFLAGQVAGSLIWIT 369

52 CASCRARPHSDFCLGCAAAPPAPFRLL------WPILGGALSLTFVLGLLSGFLVWRR 103

Oy Oy 15, Appl 2, Appli 15, Appl 15, Appl 15, Appl

Sequence

Seguence

Sequence 1, A Sequence 15, Sequence 2, A Sequence 15,

Appli Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Run on:

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20 ALLRSVAGEQAP----GTAPCSR-----GSSW------SADLDKCMDC 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-804-227C-10
Sequence 10, Application US/08804227C
Sequence 10, Application US/08804227C
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
COTTY: INDIANAPOLIS
                                US-08 446-363-2

US-08 446-363-2

US-08 542-634-22

US-08 547-292-22

PCT-US95-13703-22

US-09 286-529-20

US-09 286-529-17

US-08 833-963C-2

US-08 833-963C-2

US-08 833-963C-2

US-08 833-963C-2

US-08 833-963C-2

US-08 844-733-15

US-08 444-733-15

US-08 444-733-15

US-08 441-34-15

US-08 441-36-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/POCKET NUMBER: x-8231
TELECOMUNICATION INFORMATION:
TELEPHONE: 317.276-2459
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 72; 27.4%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3724 amino acids
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Best Local Similarity 27.4*
Matches 37; Conservative
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: peptide
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STATE: IN
COUNTRY: US
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204.250 Million cell updates/sec
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Sequence 37, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 12,
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Sequence 77,
Sequence 2,
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Sequence 2,
Sequence 103
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Sequence 4
Sequence 4
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                                                                                                                                                                                                                                                             1 MARGSLRRLLRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX
                                                                                                                                      March 12, 2002, 09:55:03; Search time 12.56 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-804-227C-10
US-08-804-198-4
US-09-5258-104
US-08-775-009-37
US-09-383-00204-2
US-09-413-814-90
US-09-413-814-77
US-09-413-814-77
US-08-440-228-2
US-08-440-400-405-08-460-537A-103
US-08-469-537A-103
US-08-944-468A-40
US-08-944-468A-40
US-08-944-468A-40
US-08-944-468A-40
US-08-944-468A-40
US-08-944-468A-40
US-08-944-466-40
US-08-944-466-40
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                                                                                                                                                                                                                                                                                                                                                               212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Result

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Query Match
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                           628 LS----PYVDWNLADVLRGAPAAPGLDRVDVVQPATFAVMVGLAALWRSLGVEPAAVIGH 683
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  ---LWPILG---
                                                                                                                                                                                                                                                                              APPLICANT: Burgett, Stanley G.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
IIILE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.8%; Score 72; DB
Best Local Similarity 27.4%; Pred. No. 42;
Matches 37; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PAUL R. CANTRELL 1:
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                 Sequence 4, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORREY AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECHMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 4:
53 ASCRARPHSDFCL----GCAAAP--
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                                                                                                                    684 SOGEIAAACVAGALS 698
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                                                                              84 --GALSLTFVLGLLS 96
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ADDRESSEE: PAUL R. C
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ZIP: 46285
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APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDF 63
General incorrections of the policy of the policy of the policy of the policy in the policy of the policy in the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 4; Length 215;
Pred. No. 3.4;
8; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/08775009
Patent No. 5935783
GENERAL INFORMATION:
APPLICANT: Gong, Weilong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CLGCAAAPPAPFRLL----WP 80
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illarity 31.7%;
Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 26; Conserve
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ZIP: 19103
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US-08-775-009-37
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181 GVPALQLHLHWGAAGRPGSEHTVEGHRFPAEIHVVHLSTAFARVDEALGRPGGLAVLAPF 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 WLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH-----SDFCLGCA 68
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                                                                                           Sequence 2, Application PC/TUS9302024

GENERAL INFORMATION:
APPLICANT: CIBA Corning Diagnostics Corp.
APPLICANT: Institute of Virology
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
CITY: San Francisco
STRATE: CA
COUNTRY: USA
ZIP- F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS .
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
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11.3%; Score 68.5; DE
Best Local Similarity 23.8%; Pred. No. 8.5;
Matches 31; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CS PV-709-92
FILING DATE: 10-WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/964,589
FILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/02024
FILING DATE: 19930308
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 AAPPAPFRLLWPILG--GA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                              101 WRRCRRERSS 110
                                                                         | | | | | | :: | 241 WRRARKKTVS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                   33; Gaps
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                                                                                                                                                                                                                                                                               45 AGROSPAKPEEPGAPEAAPCA------CCCCGGPRAAP----GGPPEAAAGLGAR 89
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                                                                                                                                                  Score 68.5; DB 2; Length 205;
Pred. No. 3.6;
6; Mismatches 31; Indels 3
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Sequence 2, Application US/07964589
Sequence 2, Application US/07964589
Sequence 2, Application US/07964589
Sequence 2, Application US/07964589
SERICANT: APPLICANT: APACTION:
APPLICANT: PASTOTEK, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/964,589
FILING DATE: 19921021
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Lauder, Leona L
REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REFRENCE/POCKET UNMBER: D-0021
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                              77 LLWPI-LGGALSLTFVL----GLLSGFL---VWRRCRRERS 109
                                                                                                                                                                                                                                                                                                                                                                      90 LAWPLRLGPAVPLSLGAPAGGSGALPGAVGPGSORRTRRHRT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 AAPPAPFRLLWPILG--GA----
                                                                                                                                                  Ouery Match
11.3%;
Best Local Similarity 31.4%;
Matches 32; Conservative
: 205 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 429 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-775-009-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-07-964-589-2
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COMPUTER READABLE FORM:
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  LENGTH:
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; Patent No. 5759863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
COGANISM: Sorangium cellulosum
US-09-413-814-77
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: HOFIE, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.1%
Best Local Similarity 24.3%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Bloecker, Helmut
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brandt, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
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US-08-442-248-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Bruin A
APPLICANT: Dougherty, Bruin A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23536
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1998-10-07
EARLIER FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSS------WSADLDKCMDCASCRAR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VMLLGAVLLLLLSGASAQEPPRVGCSEYTNRSCEECLRNVSCLWCNENKACMDYPVRKIL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 PHSDFCLGCAAAPPAPFRLLWPILGGALSLTFVLG--LLSGFLV--WRRCRRERSSPP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                             APPLICANT: MITISON, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: Compounds for their use
FILE REFERENCE: 11000.1037c1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastsEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 67.5; D
24.3%; Pred. No. 8.9;
Live 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 67.5; 25.4%; Pred. No. 3.
Sequence 12, Application US/09383586
Patent No. 6242419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 90, Application US/09413814 Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity, 24.39
Matches 25; Conservative
                                                                                                                APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bloecker, Helmut
                                                                      APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 30; Conserv
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mouse US-09-383-586-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-413-814-90
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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QQ ō. -GTAPCSR-

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for enzymatic synthesis of polyketide or
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                                                                                                                                                                                                                                                         APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GTAPCSR----
                             44 ADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPIL--GG 84
44 ADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPIL--GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic s;
TITLE OF INVENTION: DNA sequences for enzymatic s;
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
BARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Caras, Ingrid W.
APPLICANT: Caras, Ingrid W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
WIMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
ATREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 67.5; DI 24.3%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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273 PPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQVCRPGFFKASPHSQTCSKC---PP 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DCASCR----ARPHSDFCLGCAAAPP 72
                                                                                                                                                                                                                                                              31 PGTAPCSRGSSWSADLDKCM------DCASCR-----ARPHSDFCLGCAAAPP
                                                                                                                                          Score 67; DB 1; Length 928;
Pred. No. 30;
1; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                         RESULT 12
US-08-486-449-2
| Sequence 6, Application US/08486449
| Patent No. 6, Application US/08486449
| Patent No. 6, Application US/08486449
| Patent No. 6, Application US/08486449
| TILE OF INFORMATION:
| APPLICANT: Caras, Ingrid W. APPLICANT: Caras, Ingrid W. APPLICANT: Winslow, John W. ITLE OF INVENTION: AL.1 Neurotrophic Factor NUMBER OF EXQUENCES: 18
| CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/486,449
FILING DATE: 06-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING APPLICATION NUMBER: 37 OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOCCHIA, TIMOCHY E.
REGISTRATION NUMBER: 35 700
REFERENCE/DOCKET NUMBER: P0920P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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1; Mismatches
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Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 31.6%;
Matches 18; Conservative 1
                                                                                                                                             Query Match
Best Local Similarity 31.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 PGTAPCSRGSSWSADLDKCM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                     ; TOPOLOGY: linear US-08-440-815-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-469-537A-103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Grass, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: Gouth San Bruno Blvd
CITY: South San Francisco
STRATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAIL (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 1
Pred. No. 30;
1; Mismatches
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTONNEY, AGENT INFORMATION:
NAME: TOTCHA, TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELEPHONE: 415/25-8674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELECHONE: 415/25-8674
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FILING DATE: 15-MAY-1995
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128

FILING DATE: 27-0CT-1994

ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, Timothy E.
REGISTRATION NUMBER: 36/700

REFERENCE/DOCKET NUMBER: 920C1

TELECOMMUNICATION INFORMATION:
TELEFRAX: 415/225-981

TELEFAX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08440815
Patent No. 5798448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 31.6%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 928 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-442-248-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-440-815-2
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Sequence 40, Application US/08599654
Fatent No. 5882925
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
TITLE OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1311 KMDHSCRACEDGYRLENETCMSCPFGLGGLNCGNPYQLITVVIAAAGGGLLL--ILGIA- 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 ----SCRA-----RPHSDFCLGCAAPPA-----PFRLLWPIL---GGALSLTFVLGLLS 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.0%; Score 67; DB 2; Length 148 Best Local Similarity 24.1%; Pred. No. 51; Matches 32; Conservative 18; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GSLRRLLRLLVLGLWLALLRSVAGEQAPGTAP-CSRGSSWSADLDKCMDCA-
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PatentIn Release #1.0, Version #1.30
                                                                                                            FILING DATE: 09-FEB-1996
PRIOR APPLICATION NUMBER: US 08/485,573
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-UN-1995
PROR APPLICATION NUMBER: US 08/386,844
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY AGENT INFORMATION:
NAME: CORUZI, LADRA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 36,742
RELEPHONE: (212) 869-8864
TELEFAX: (212) 869-8864
ITELEFAX: 6614 PENNIE
INFORMATION FOR SEO ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,654
FILING DATE: 09-FEB-1996
CTASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
  APPLICATION NUMBER: US/08
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-616-844-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1368 -- LIVICCRKNKN 1378
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-599-654-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   р
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 PPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQVCRPGFFKASPHSQTCSKC---PP 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score 67; DB 2; Length 1005; 31.6%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                  ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
OOFWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
RESTREMLE/DOCKET NUMBER: 32,143
REFERENCE/DOCKET NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08616844
Patent No. 5849578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 103: SEQUENCE CHARACTERISTICS:
  KINASES
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1005 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 31.6
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALB, DEAN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 914-345-74 | TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-469-537A-103
                        NUMBER OF SEQUENCES: 1
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                     U.S.A.
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ZIP: 10036-2711
                                                                                                  TOPOLOGY:
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APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATORNEY/AGENT INFORMATION:
NAME: CORDZI, LAURA A
REGISTRATION NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1481 amino acids
STRANDEDNESS:
MOLECULE TYPE: protein
US-08-599-654-40
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 Query Match
 11.0%;
 Score 67;
 DB 2;
 Length 1481;

 Best Local Similarity 24.1%;
 Pred. No. 51;
 An Edit of the conservative 18;
 An Edit of the conservative 18

8

97 GFLVWRRCRRERS 109

|: ||: ||: 1368 --LIVTCCRKNKN 1378

QQ

ag.

Search completed: March 12, 2002, 09:57:13 Job time: 130 sec

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608
1 MARGSLRRLIRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/USO92_COMB.pep:*
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3148936 segs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

g	60, Appl	59, Appl	627, App	265, App	16, Appl	220, App	4, Appli	627, App	Sequence 4, Appli
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence
SUMMARIES	PCT-US98-10868-60	US-09-189-144-59	US-09-307-140-627	US-09-316-633-265	US-09-445-258-16	US-09-465-587-220	US-09-742-454A-4	US-09-817-076-627	US-09-883-777-4
DB	-	15	17	17	18	18	21	22	22
% Query re Match Length DB 1	114	114	129	129	129	129	129	129	129
% Query Match	99.8	8.66	93.9	93.9	93.9	93.9	93.9	93.9	93.9
Score	607	607	571	571	571	571	571	571	571
Result No.	7	7	3	4	2	9	7	80	6

NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ006PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504

V44440444444440880	Sequence 2, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 136, App Sequence 139, App Sequence 284, App Sequence 225, App Sequence 228, App Sequence 228, App Sequence 228, App Sequence 20145, App Sequence 20145, Appli Sequence 20163, Appli Sequence 210, Appli Sequence 210, Appli Sequence 210, Appli Sequence 210, Appli Sequence 218, Appli Sequence 5, Appli	Sequence 3, Appliance 159, Appliance 1721, Appliance 1721, Appliance 1393, Appliance 26, Appliance 11, Appliance 11, Appliance 11, Appliance 11, Appliance 11, Appliance 12, Appliance 11, Appliance 12, Appliance 12, Appliance 16, Appliance 1	
10 571 93.9 129 24 11 450 74.0 129 21 13 433 71.2 309 22 14 433 71.2 309 22 15 274.5 45.1 112 18 18 274.5 45.1 112 18 20 274.5 45.1 112 18 21 274.5 45.1 112 18 22 274.5 45.1 112 18 23 88.5 14.6 400 16 24 88.5 14.6 400 16 25 87.5 13.2 426 11 274.5 45.1 156 12 28 87 14.3 426 11 27 27.5 45.1 156 18 28 87 14.3 426 16 29 88.5 14.6 526 17 29 88.5 14.6 526 17 29 88.5 13.2 268 5 31 80.5 13.2 268 5 32 80.5 13.2 268 5 33 80.5 13.2 268 5 34 80.5 13.2 508 5 35 80.5 13.2 508 5 36 80.5 13.2 508 5 37 14.3 426 18 38 80.5 13.2 508 5 38 80.5 13.2 508 5 39 79 13.0 194 21 42 77 12.7 12.7 448 20 43 80.5 13.2 508 5 34 80.5 13.2 508 5 35 80.5 13.2 508 5 36 80.5 13.2 508 5 37 12.6 250 17 42 77 12.7 12.7 448 20 41 77 12.7 12.7 448 20 42 77 12.7 12.7 448 20 43 80.5 13.2 508 5 36 80.5 13.2 508 5 37 80.5 13.2 508 5 38 80.5 13.2 508 5 38 80.5 13.2 508 5 39 79 13.0 194 21 42 77 12.7 12.7 448 20 43 76.5 12.6 250 17 44 76.5 12.6 250 17 45 76.5 12.6 250 17 47 12.7 12.7 12.7 488 60 5 13.2 508 5 35 80.5 13.2 508 5 36 80.5 13.2 508 5 37 80.5 13.2 508 5 38 80.5 13.2 508 5 39 79 13.0 194 21 40 77 12.7 12.7 448 76.5 12.6 250 17 42 77 12.7 12.7 448 76.5 12.6 250 17 42 77 12.7 12.7 12.7 12.7 12.7 12.7 12.7		US-08-173-512-3 US-08-173-512-3 US-09-859-500-159 US-05-311-261-139 PCT-US01-08631-56652 US-09-674-330A-3 US-09-674-330A-3 US-09-322-409-31 US-09-322-409-31 US-09-322-409-26	C., et Inc.
10 571 93.9 129 11 450 74.0 129 12 433 71.2 309 13 433 71.2 309 14 433 71.2 309 15 379.5 65.4 300 16 274.5 45.1 112 17 274.5 45.1 112 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 27 4.5 45.1 115 28 8.5 14.6 400 29 88.5 14.6 400 29 88.5 14.6 400 29 88.5 14.6 400 29 88.5 14.6 400 29 88.5 14.0 73 21 274.5 45.1 115 29 88.5 14.6 400 29 88.5 14.6 400 29 88.5 13.2 426 31 80.5 13.2 508 31 80.5 13.2 508 32 80.5 13.2 508 33 80.5 13.2 508 34 80.5 13.2 508 35 80.5 13.2 508 36 80.5 13.2 508 37 80.5 13.2 508 38 80.5 13.2 426 39 79 13.0 194 40 77 12.7 448 41 76.5 12.6 250 44 76.5 12.6 250 44 76.5 12.6 250 44 76.5 12.6 250 45 77 12.7 12.7 152 47 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 250 49 70 13.0 194 40 77 12.7 12.7 152 41 76.5 12.6 250 42 77 12.7 12.7 12.7 12.7 42 77 12.7 12.7 12.7 42 77 12.7 12.7 12.7 42 76.5 12.6 250 44 76.5 12.6 250 45 76.5 12.6 250 46 76.5 12.6 250 47 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 250 48 76.5 12.6 276 49 76.5 12.6 276 40 77 12.7 12.7 12.7 41 76.5 12.6 276 41 76.5 12.6 276 42 76.5 12.6 276 43 76.5 12.6 276 44 76.5 12.6 276 45 76.5 12.6 276 47 76.5 12.6 276 48 7 14.3 30 48 70.5 12.6 20 48 70.6 12.6 12.6 20 48 70.6 12.6 1	444444 8 8 8 86466 4466 68	4 0 C & C	SCJ/TUS Borne (1) Borne (2) Borne (3) Borne (3) Borne (4)
RESULT 1	1229 1229 1229 1229 1229 1229 1229 1229	2000 1101 1100 1100 1100 1100 1100 1100	ttion PC 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
110 450 111 450 112 4530 113 4531 114 450 115 379.5 116 274.5 120 274.5 121 274.5 122 28 87.5 123 88.5 124 88.5 125 88.5 127 80.5 128 80.5 128 80.5 128 80.5 128 80.5 128 80.5 128 80.5 129 88.5 120 88.5		1 M M M M M M M M M M M M M M M M M M M	60 Applice ORMATION ORMATION INVENTIC SEQUENC DENCE AL BATYLOR ROCKVILL ROCK READOR READOR READOR ROCK READOR ROCK ROCK ROCK ROCK ROCK ROCK ROCK RO
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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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                                                                                                                                     Sequence 627, Application US/09307140
; GENERAL INFORMATION:
    APPLICANT: Gearing, David P.
    APPLICANT: Gearing, David P.
    APPLICANT: Robison, Keith E.
    TITLE OF INVENTION: Nucleic Acid Molecules Derived from a TITLE OF INVENTION: Human Aortic Endothelium Library FILE REFERENCE: MLN98-14PA
    CURRENT APPLICATION NUMBER: US/09/307,140
    CURRENT FILING DATE: 1999-05-07
    EARLIER FILING DATE: 1998-05-07
    NUMBER OF SEQ ID NOS: 1168
    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 265, Application US/09316633
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Human Mesangial Cell Library
FILE REFERENCE: MLN98-16pp.
CURRENT APPLICATION NUMBER: US/09/316,633
CURRENT FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%; Score 571; DB 17; 94.7%; Pred. No. 1.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/087,052 PRIOR FILING DATE: 1998-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7
Matches 107; Conservative
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(27)
US-09-307-140-627
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US-09-316-633-265
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                                                                                                                        US-09-307-140-627
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LENGTH: 129
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LENGTH: 129
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                                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                        99.8%; Score 607; DB 1; I
100.0%; Pred. No. 4.7e-51;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-09-189-144-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 32 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-11-10

CURRENT FILING DATE: 1998-11-10

EARLIER FILING DATE: 1998-11-10

EARLIER FILING DATE: MAY 28, 1998

EARLIER FILING DATE: MAY 30, 1997

EARLIER PELLING DATE: MAY 30, 1997

EARLIER PELLING DATE: AUGUST 29, 1997

EARLIER FILING DATE: AUGUST 29, 1997

NUMBER OF SEQ ID NOS: 229

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 59, Application US/09189144; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steven M. Ruben, et al
                                      ; TYPE: amino acids ; TOPOLGS: TOPOLGS: 1000 acid ; TOPOLGS: 1near ...
TELEFAX: (301) 309-8439 .
INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     Query Match 99.8%
Best Local Similarity 100.0
Matches 113; Conservative
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Matches 113; Conservative
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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                           1 MARGSLRRLILVILVILVILVILALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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GURERAL INCOMATION:
APPLICANT: Kato, Seishi
APPLICANT: Kato, Seishi
APPLICANT: Kato, Seishi
APPLICANT: Kimura, Tomoko
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
TITLE OF INVENTION: HUMAN PROTEINS ENCODING THESE PROTEINS
FILE REFERENCE: GIN-6706CPUS
CURRENT APPLICATION NUMBER: US/09/445,258
CURRENT FILING DATE: 1999-12-01
PRIOR PRILING DATE: 1999-12-01
PRIOR PAPLICATION NUMBER: PCT/US98/02445
PRIOR APPLICATION NUMBER: JP 9-144948
PRIOR FILING DATE: 1997-06-03
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                                                                                      61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                             61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN ADULT EPIDERMAL KERATINOCYTE LIBRARY
FILE REFERENCE: 1600.1080-001
CURRENT APPLICATION NUMBER: US/09/465,587
CURRENT FILING DATE: 1999-12-17
PRIOR FILING DATE: 1998-12-31
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Pred. No. 1.7e-47;
0; Mismatches 6;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 220
LENGTH: 129
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 129
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Best Local Similarity 94.7%;
Matches 107; Conservative
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; LOCATION: (1)...(27)
US-09-465-587-220
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APPLICANT: Holizman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a TITLE OF INVENTION: Human Aortic Endothelium Library FILE REFERENCE: MLN98-14pa
CURRENT APPLICATION NUMBER: US/09/817,076
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 09/307,140
PRIOR APPLICATION NUMBER: 60/084,565
PRIOR APPLICATION NUMBER: 60/084,565
PRIOR FILING DATE: 1999-05-07
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Pred. No. 1.7e-47;
0; Mismatches 6;
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FILE REPERENCE: 2968 B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/172,878
PRIOR APPLICATION NUMBER: 60/172,878
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-05-10
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0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 627
LENGTH: 129
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APPLICANT: Gearing, David P.
                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09742454A GENERAL INFORMATION:
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Best Local Similarity 94.7%;
Matches 107; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 107; Conserv
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ORGANISM: Mus sp.
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                                                                                                                                                                                                                   93.9%; Score 571; DB 22; Length 129; llarity 94.7%; Pred. No. 1.7e-47; Conservative 0; Mismatches 6; Indels (
                                                        Length 129;
                                                                                         Indels
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; GENERAL INFORMATION:
    APPLICANT: Hillman, Jennifer L.
    APPLICANT: Hall, Preeti
    APPLICANT: Tang, Y. Tom
    APPLICANT: Yee, Henry
    APPLICANT: Baughn, Mariah R.
    TILE OF INVENTION: HUMAN MEMBRANE-SPANNING PROTEINS
    TITLE OF INVENTION: HUMAN WEMBRANE-SPANNING PROTEINS
    TORRENT APPLICATION NUMBER: US/60/109,869
    CURRENT APPLICATION NUMBER: US/60/109,869
    CURRENT PILING DATE: 1998-11-24
    NUMBER OF SEQ. ID NOS: 34
    SOFTWARE: PERL PROGram
    SEQ. ID NO 2.
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                                                    Score 571; DB 22;
Pred. No. 1.7e-47;
0; Mismatches 6;
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FILE REFERENCE: 2968-C
CURRENT PAPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-05-10
PRIOR PELING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
SEQUENCE: SEQUENCE: 2000-12-19
NUMBER OF SEQUENCE: 2000-12-19
NUMBER OF SEQUENCE: 2000-12-19
SEQUENCE: SEQUENCE: 2000-12-19
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                                                      93.98;
94.78;
                                                  Query Match 93.9
Best Local Similarity 94.7
Matches 107; Conservative
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CORGANISM: homo sapiens
US-09-883-777-4
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107; Conserv
US-09-817-076-627
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US-60-109-869-2
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Best Local Si
Matches 107;
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                                                                                                                  Length 129;
                                                                                                                                                                 Indels
                                                                                                                Score 571; DB 24;
Pred. No. 1.7e-47;
0; Mismatches 6;
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GENERAL INFORMATION:
APPLICANT: WILEY, Steven R.
TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT PILING DATE: 1090-12-19
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/212,878
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR PELLING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
PRIOR PELLING DATE: 2000-12-19
PRIOR PELLING DATE: 2000-12-19
PRIOR PELLING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
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                                                                                                                93.98;
; FEATURE: -
; OTHER INFORMATION: 2454048
US-60-109-869-2
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US-09-883-777-9
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                                                                                                                                                                                                                                                  1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: human TWEAK OTHER INFORMATION: receptor fusion protein construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.2%; Score 433; DB 21; Length 309; ilarity 74.1%; Pred. No. 1.2e-33; Conservative 2; Mismatches 5; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----WRSCDKTHTCPP 90
                                                                                                                                                                   Length 129;
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                                                                                                                                                                 Score 450; DB 22;
Pred. No. 1.1e-35;
                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09742454A
GENERAL INFORMATION:
APPLICANT: WILLEY, SEVEN R.:
TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/212,878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.0
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GENERAL INFORMATION:
APPLICAMT WILEY, Steven R.
TITLE OF INVENTION: TWEAR RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT APPLICATION NUMBER: US 60/172,878
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR PILING DATE: 2000-05-10
PRIOR PLING DATE: 2000-05-10
                                                                                                                                                                 74.0%;
75.2%;
SOFTWARE: PatentIn version 3.1
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Best Local Similarity
Matches 85; Conserv
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Matches 83; Conserv
                                                                              : ORGANISM: Mus sp. US-09-883-777-5
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US-09-742-454A-7
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                                        LENGTH: 129
TYPE: PRT
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LENGTH: 309
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                     SEQ ID NO 5
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US-09-883-777-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9
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----WRSCDKTHTCPP 90
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Pred. No. 1.2e-33;
2; Mismatches 5;
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ilarity 88.0%; Pred. No. 1.8e-28;
Conservative 0; Mismatches 1.
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GENERAL INFORMATION:
APPLICANT: WILEY, Steven R.
TITLE OF INVENTION: TWEAR RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT APPLICATION NUMBER: US 60/172,878
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR PRICATION NUMBER: US 60/203,347
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 9
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Job time: 197 sec
                           09/742,454
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PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/;
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 309
                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                          Query Match 71.2%;
Best Local Similarity 74.1%;
Matches 83; Conservative
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Best Local Similarity
Matches 73; Conserv
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Search time 16.7 Seconds (without alignments) 404.970 Million cell updates/sec
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/cgn2_6/ptodata/2/paa/JUSO_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/JUSO_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/JUSIO_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/JUSIO_NEW_COMB.pep:*

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Pending_Patents_AA_New:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, App. Sequence 55653, A Sequence 65653, A Sequence 46575, A Sequence 5113, A Sequence 3, Appli Sequence 74, Appl Sequence 227, App Sequence 2573, App Sequence 254, App Sequence 258, App Sequence 80730, A Sequence 80730, A Sequence 8, Appli Sequence 2, Appli Sequence 65652, A Sequence 46576, A Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-690-454-59 US-10-062-599-59 US-10-062-599-59 US-09-708-427-65653 US-09-708-427-65652 US-09-708-427-6575 US-09-708-427-6575 US-09-708-427-6575 US-09-708-427-6575 US-09-708-427-6573 US-09-674-256A-227 US-09-674-256A-227 US-09-604-693A-254 US-09-604-693A-254 US-09-708-427-48572 US-09-604-693A-254 US-09-708-427-48772 US-09-604-693A-254 US-09-708-427-80730 US-09-708-427-80730 US-09-674-554-254 US-09-674-554-254 US-09-674-554-254 US-09-674-554-2 US-09-989-723-231 US-09-989-724-231 US-09-989-730-231 US-09-990-436-231 SUMMARIES DB Length 146 242 242 242 365 365 89 461 720 720 720 720 Query 144.1 144.1 123.3 133.8 123.3 607 607 87 86 86 84 84 77 77 73 22777 2882 20000 20000 20000 20000 20000 20000 Score Result Ñ.

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61 SDFCLGCAAAPPAAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor FILE REFERENCE: 00-103
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100.0%; Pred. No. 6.6e-57;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59
                                                                                                                                                                                                                                                APPLICANT: Steven M. Ruben, et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
FILE REFERENCE: P2006P1
                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PZ00PLI
CURRENT PELLING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 09/460,454
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/056,256
PRIOR APPLICATION NUMBER: 60/056,296
PRIOR PRILING DATE: AUGUST 29, 1997
PRIOR FILING DATE: AUGUST 29, 1997
                                                                                                                                                                                       ; Sequence 59, Application US/10062599; GENERAL INFORMATION:
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Matches 113; Conservative
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                                                                                                                                         RESULT 2
US-10-062-599-59
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Sequence 65653, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID:
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VETSION 3.1
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GENERAL INFORMATION
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
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                                                                                                                                                                                                                                                                                                                              Gaps
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CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ); OTHER INFORMATION: Ceres Seq. ID 1929197
US-09-708-427-65653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 TFVLGLLSGFLVWRRCRR--ERS-SPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ALALASP----KRSRRKNERSASPPP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays subsp. mays
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                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-008-063-2
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LOCATION: 1..153
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LOCATION: 1..153
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Best Local Similarity
Matches 31; Conserva
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: 1716-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILIG DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 65113
LENGTH: 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCM---DCASCRA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LCCATION: 1..123
; OTHER INFORMATION: Ceres Seq. ID 1852550
US-09-708-427-46575
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US-09-708-427-65113
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                                                                                                                   Sequence 46575, Application US/09708427 GENERAL INFORMATION:
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LOCATION: 1..123
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LENGTH: 123
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GENRRAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCM---DCASCRA 57
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TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
1.0CATION: 1..163
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
1.0CATION: 1..163
COTHER INFORMATION: Ceres Seq. ID 1929196
US-09-708-427-65652
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; LCCATION: 1..107
; OTHER INFORMATION: Ceres Seq. ID 1852551
US-09-708-427-46576
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Best Local Similarity 35.2%:
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                                                                                                                                      SEQ ID NO 65652
LENGTH: 163
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LENGTH: 107
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APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: GLAXO GROUP LIMITED
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: PCT/US01/49232
CURRENT APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-01-09
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                  PRIOR FILLING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                          Pred. No
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  FILING DATE: 2001-03-19
APPLICATION NUMBER: 60/281,535
FILING DATE: 2001-04-04
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ilarity 27.9%;
Conservative
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                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-49232-74
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Best Local Similarity
Matches 29; Conserva
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                 SEQ ID NO 74
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TITLE OF INVENTION: A novel polypeptide, a cDNA encoding the polypeptide and utilizat
TITLE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE REPERBUCE: Q61531
CURRENT APPLICATION NUMBER: US/09/674,379A
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: PCT/JP99/02284
PRIOR APPLICATION NUMBER: JP 10-119731
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEC ID NOS: 17
SOFTWARE: Patentin version 3.1
SEC ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
; OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart
US-09-674-379A-3
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                                                                            39 GSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLL--S 96
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                                                                                                                 15 GSSVPASLISPL--LKCRARINRQDPWCYSPVPFRPFPPFWSLGGGTLHLRLRLGVLQRS 72
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Pred. No. 1.5;
8; Mismatches 24; Indels
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GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GFS0039
CURRENT APPLICATION NUMBER: PCT/US01/49232
CURRENT APPLICATION NUMBER: PCT/US01/49232
CURRENT FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/276,988
Best Local Similarity 35.1%; Pred. No. 1.5; Matches 27; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09674379A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.78;
24.18;
                                                                                                                                                                                 97 GFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                73 AFLSWLLVRRSMAKDYP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.1
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
PCT-US01-49232-74
                                                                                                                                                                                                                                                                                                                                  US-09-674-379A-3
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1;

S

Page

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20; Gaps

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Indels
                                                                                                                        69 AAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                 188 VSRPTEKSLLMLFLWAVGALSFLLGLADLVCSLRRRRRRPGPP 231
  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
11.9%; Score 72.5; DB 5;
Best Local Similarity 26.4%; Pred. No. 1.5;
Matches 23; Conservative 11; Mismatches 46;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/604,693A CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1...146
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1...146
COTHER INFORMATION: Ceres Seq. ID 1855339
US-09-708-427-48572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 LSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 254, Application US/09604693A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Corynebacterium glutamicum
US-09-604-693A-254
                                                                                148 LLRTLLEAAFGALHYFLFGFLAPKKFPCT
  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pompejus, Markus
  29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                               US-09-708-427-48572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-604-693A-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                           APPLICANT: SCHMITT, ARIND
APPLICANT: SCHMITT, ARIND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: BOBLY.
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PANCREAS TUMOR TISSUE
FILE REFERENCE: ALBRE 3
CURRENT APPLICATION NUMBER: US/09/674,266A
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 661
SOFTWARE: PATELITY OF 1.
SEQ ID NO 227
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---FCLGCAAAPPAPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRIMERS FOR SYNTHESIS OF FULL LENGTH CDNAS TITLE OF INVENTION: AND THEIR USES FULL ERFERENCE: 08335/0122
FULE REFERENCE: 08335/0122
CURRENT APPLICATION NUMBER: US/09/611,526
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: JP 2000-118774
PRIOR APPLICATION NUMBER: JP 2000-118774
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 RLL----WPILG-GALSLTFVLGLLSGFLVWRRCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 RIWVHCTGWPRLATGLWPLT-----CQVWGTPRKQQPLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73; DB:
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 APGTAPCSRGSSWSADLDKCMDCASCRARPHSD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No
                Sequence 227, Application US/09674266A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2573, Application US/09611526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAKAMATSU, AI
SUGIYAMA, TOMOYASU
NAGAI, KEIICHI
KOJIMA, SHINICHI
OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%;
25.5%;
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27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OTA, TOSHIO APPLICANT: NISHIKAWA, TETSUO
                                                                                HINZMANN, BERND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 25.58
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOGAI, TAKAO
HAYASHI, KOJI
ISHII, SHIZUKO
KAWAI, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4484
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 2573
LENGTH: 370
                                                           APPLICANT: SPECHT, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOGA, HISASHI
                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-674-266A-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-611-526-2573
US-09-674-266A-227
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APPLICANT:
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APPLICANT:
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Sequence 48572, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 48572
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                 ------RPPCTGVVDCY 187
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Ostroder, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN DNA REPLICATION, PROTEIN SYNTHESIS,
TITLE OF INVENTION: AND PATHOGENESIS
FILE REFERENCE: BGI-130CP
9 LLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPILGGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 AGRRVPSPSPSSLGPQWRRRRRRRRRRAVPSSTPPTSARSFPRPASPPT-----SSLSSG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 146;
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4; Query Match 11.9%; Score 72.5; DB 5; Length 242; Best Local Similarity 30.5%; Pred. No. 2.5; Matches 18; Conservative 7; Mismatches 17; Indels 17; Gaps

δ qq Search completed: March 12, 2002, 09:59:17 Job time: 184 sec

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14.5
Compugen Ltd.
   GenCore version
Copyright (c) 1993 - 2000
```

OM protein - protein search, using sw model

March 12, 2002, 09:55:03; Search time 14.35 Seconds Run on:

(without alignments)
605.150 Million cell updates/sec

US-09-690-454-59 Title:

1 MARGSLRRLLRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	probable chitinase	probable export pr	hypothetical prote	hypothetical prote		⊐	ribonuclease (EC 3	conserved hypothet	fibrillin-1 precur	ţ	glypican precursor		hypothetical prote	Fas antigen precur	conserved hypothet	osmoregulated prol	hypothetical prote	probable protein k	diheme cytochrome	glycoprotein precu	receptor-type prot	bone marrow stroma	receptor-like tyro	receptor tyrosine	1	receptor tyrosine		hypothetical prote	conserved hypothet
a	T04484	878698	B70939	T20910	T22758	660695	T04420	D75303	A55624	T36798	I56545	D75330	C70893	JC2395	B69092	E75138	B61213	T00872	T46966	GNVUUK	150615	JC4390	S51603	S47489	S51604	S49015	98	3694	E83085
DB	7	7	7	7	~	7	7	~	7	7	7	7	7	~	Н	~1	~	7	-	-	7	7	7	~	7	7	7	7	7
% Query Match Length	332	245	436	635	768	261	227	346	2871	175	558	424	287	324	431	484	480	683	384	1008	1013	319	893	868	981	1005	389	394	549
% Query Match	12.9	12.6			12.2	12.1		•	11.8		11.5	11.4	11.4				11.2	11.2	11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0	10.9	•	10.9
Score	78.5	76.5	75.5	75.5	74	73.5	73	72.5	72	71	70	69.5	69.5	69	68.5	68.5	68	68	67.5	67.5	67.5	49	29	67	67		66.5	99	99
Result No.	Н	7	3	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

structural polypro reverse transcript	trophozoite cystei	notch 3 protein -	hypothetical prote	probable export pr	flagellar biosynth	hypothetical prote	serine/threonine-s	notch3 protein - h	conserved hypothet	hypothetical prote	protein-tyrosine-p	structural protein	hypothetical prote	probable chitinase
GNWVR3 T07965	A42125	S45306	T49381	B36869	G85812	F83545	T02731	S78549	F82989	C83407	A48148	C44212	.B82577	T03239
1 0	2	7	7	~	~	7	7	7	7	7	-	~	7	7
992	1766	2318	214	245	245	206	884	2321	196	466	1445	123	317	335
10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.6	10.6	10.6
9 9	99	99	65.5	65.5	65.5	65.5	65.5	65.5	65	65	65	64.5	64.5	64.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C; Species: Hordeum vulgare (barley)
C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 11-May-2000
C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 11-May-2000
C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 11-May-2000
C; Accession: T04484
A; Title: Identification of an enhancer/silencer sequence directing the aleurone-speci A; Reference number: 215373; MUID: 95078949
A; Reference number: 215373; MUID: 95078949
A; Reference number: 215373; MUID: 95078949
A; Mocession: T04484
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-332 < LEA>
A; Cross-references: EMBL: L34211; NID: 9576566; PIDN: AAA56787.1; PID: 9507961
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CHI33
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
E;28-69/Domain: hevein chitin-binding domain homology <HCB>
F;85-322/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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12.9%; Score 78.5; DB 2; Length 332;
Best Local Similarity 32.0%; Pred. No. 2.7;
Matches 33; Conservative 9; Mismatches 38; Indels 2
probable chitinase (EC 3.2.1.14) - barley
```

13 LVLGLWLALLRSV----AGEQAPG-TAP----CSRGSSWSADLDKCMDCASCRARPHSDF 63 d δ

64 CLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWR-RCR 105 δ

Q

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probable export protein flip precursor - Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: Ol-Feb-1999 #sequence_revision Ol-Feb-1999 #text_change 21-Jul-2000 C;Accession: S78698 R;Ohnishi, K.; Fran, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M. J. Bacteriol. 179, 6092-6099, 1997 A;Title: The Flio, Flip, Rilo, and Flik proteins of Salmonella typhimurium: putative A;Reference number: S78696; MUID:97464436 A;Accession: S78698 A;Molecule type: DNA A;Residues: 1-245 <OHNA A;Residues:

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G69099
probable pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrop C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000
                                                                                                                                                                                                                              A;Cross-references: EMBL:281503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9
A;Experimental source: clone F14F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:282083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9
A;Experimental source: clone ZK1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:281091; PIDN:CAB03142.1; GSPDB:GN00019; CESP:F55H12.1 A;Experimental source: clone F55H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F55H12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Aatesion: T22758
R;Dobson, R.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219610
A;Reference number: 219610
A;Recession: T22758
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 PITAYKNGGLSF---LIAYVVCGILFAVPAIHMEFALGOYAAKSPPAAFRRMMPILEGVG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PGTAPCSRGSSWSADLDKCMDCASCRARP--HSDFCLG--CAAAPPAPFRLLWPILGGAL 86
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C;Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASCRARP - - HSDFCLG - - CAAAPPAPFRLLWPILGGALSLTFVLGLLSG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T27646
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316/3; 403/1; 444/3; 547/3;
                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                      R;Gardner, A.
submitted to the EMBL Data Library, November 1996
                  submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%; Score 75.5; DI 36.6%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%; Score 74; DB
llarity 40.0%; Pred. No. 14;
Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Conservative
                                             A; Reference number: Z19345
A; Accession: T20910
                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z20398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ::| : |
149 WMTCLVGAIIG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 SLTFVLGLLSG 97
                                                                                                                                                          A; Molecule type: DNA A; Residues: 1-635 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 3
A; Introns: 71/3; 184/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A: Residues: 1-768 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-635 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: ZK1010.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: F55H12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 20;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
By0939
Hypothetical protein Rv0246 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-U1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C; Accession: B70939
R; COle, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davise, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, S.; Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-436 <COLD-A; Residues: Res
                                                                                   be involved in export of flage
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hypothetical protein ZK1010.9 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C.Accession: T20910; T27646
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LRRLLRLLVLGLWLALLRSVAGEQAPG - TAP - CSRGSSWSADLDKCMDCASCRARP - - 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGSLRRLLRLLVLGLWLALLRSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PILGG------ 84
                                                                                                                                                                                                                                  predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 12.6%; Score 76.5; DB 2; Length 245; Local Similarity 30.8%; Pred. No. 3.3; nes 33; Conservative 9; Mismatches 38; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 --HSDF------CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
A;Gene: flip
C;Function:
G;Function:
A;Description: may be involved in flagellar assembly; may k
C;Superfamily: flagellar biosynthetic protein
C;Keywords: flagellum; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-245/Product: probable export protein flip #status pred
F;45-61/Domain: transmembrane #status predicted <TM1>
F;89-105/Domain: transmembrane #status predicted <TM2>
F;89-205/Domain: transmembrane #status predicted <TM3>
F;189-205/Domain: transmembrane #status predicted <TM3>
F;212-228/Domain: transmembrane #status predicted <TM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ALSLTFVLGLLSGFLVWRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AVPGDQPDEVVAVVLFVCVGLLGGIALWNRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARPHSDFCLGCAAAPPAPFRLLW-
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Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 33;
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3;

Gaps

7;

Indels

Length 635;

g òγ q 3

Gaps

4;

Length 768;

22

g δ qq δ g

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36 CSRGSSWSADLDKCMD-
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Matches 3
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C; Accession: G69099
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; (21u, D.).; Spadafora, R; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514
A.Accession: 669099
A; Reference number: A69009; MUID:98037514
A; Accession: 669099
A; Reference number: A69009; MUID:98037514
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Wolecule type: DNA
A; Residues: 1-261 < WHT>
A; Roperimental source: strain Delta H
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Reywords: coenzyme A; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75303
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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R. Rogers, J.C.; Rogers, S.W.
Submitted to the EMBL Data Library, April 1997
A. Reference number: 21535
A. Accession: T04420
A. Accession: T04420
A. Accession: T04420
A. Residues: preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-27 < ROG>
A. Across-references: EMBL.AF000940; NID:g2150001; PIDN:AAB58719.1; PID:g2150002
A. Experimental source: cv. Igri
C. Genetics: 35/3; 87/3
C. Superfamily: Enterobacter ribonuclease
C. Reywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr_1999 #sequence_revision 23-Apr-1999 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 PGTAPCSRGSSWSA-----DLDKCMDCASCRA-----RPHS---DFCLGCA-AAPPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LLRSVAGEQAPGTAPCSRG-SSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73.5; Di
Pred. No. 6.6;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonuclease (EC 3.1.-.-) - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 29.2 tes 19; Conservative
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : :
251 PVKAI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 PFRLL 78
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Best Local S
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W.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: D75303
A;Accession: D75303
A;Accession: D75303
A;Accession: D75303
A;Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646
A;Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646
A;Gene: DR2205
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C.Species: Mus musculus (house)
C.Species: Mus mouse (house)
A.Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin A.Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin A.Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin A.Tecesion: AS5624; MulD:95130561
A.Molecule type: mRNA
A.Molecule type: MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transcription regulator soxR-like - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 C;Accession: T36798 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, July 1999 A;Reference number: Z21614 A;Reference number: Z21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| :| :| || :| || 87 LLVTCYGLGVL--TAGSASPWTV-----MWVGALVAAFGAVLATVWHLRPAGSLFFVFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC---RARPHSD----FC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- DFCLGC 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LGCAAA--PPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 58;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 72.5; 28.8%; Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2100 PTEPDEAFRQICPFGSGII 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.8
Best Local Similarity 25.3
Matches 20; Conservative
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Gaps

25;

35; Indels

DB 2;

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Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandraam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Accession: C70893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-424 < WHI>
A; Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645
A; Experimental source: strain Rl
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A;Cross-references: GB:AL021897; GB:AL123456; NID:93256022; PIDN:CAA17185.1; PID:9289
                                                            C;Species: Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75330
C;Accession: D75330
M; Shen, M; Vamathevan, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M; Shen, M; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number, A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 AATPOTPEPOPIRSTWWIRHYTFTGTAMGLVFVWFSMTPSLLPRGPLFQGLVSGICGAFG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA---- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RGIIRLILALLLIG---AGINACRNREAQDIAPPAAAAAQSQAAPRKAASASSPAPTATE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Rv1069c - Mycobacterium tuberculosis (strain H37RV)
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1069c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PAVSAPAADGCLPAAPAVTQAPRPPQP-----LSGRLGL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 ----RPHSDFCLGCAAA-----PPAPFRLLWPILGGALSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.5; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 YGLGVFAVWLVRYMRSHNSSPPP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.4%; 29.7%;
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Best Local Similarity
Matches 30; Conserv
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: D75330
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A;Gene: DR1985
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195646

C.Species Ratius norvegicus (Norway rat)

R.Accession: 155645, JC1281, PC132

R.Attlework, E.D.; Stipp C.S.; Kumbasar, A.; Lander, A.D.

A.Accession: 155645

A.Accession: 155845

A.A
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-175 < OLI>
A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI30A.18c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 70; DB 2; Length 558; 37.7%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                         DB 2; Length 175;
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                                                                                                                                                                                                                                                                                                                                                                                             33;
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-----GCLSLETCVL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 SCRARPHSDFCLGCAAAPPAPFRLLWPILGGALSL-TFVL 92
                                                                                                                                                                                                                                                                                                                      11.7%; Score 71; DB 29.0%; Pred. No. 8.4; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | |:||
109 N-RLRDHLTDCIGC-----
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.0°
Matches 29; Conservative
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Gaps

37;

Indels

17;

Length 587;

DB 2;

5

27; Gaps

27; Indels

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332 WSGDVRPVHHPERCTDCAVCLAARRCPTHAIDNGLDLDRCFGCGVC-----AWSCPSG 384
                                                                                                         42 WSADL-----DKCMDCASC----RARPHS------DFCLGCAAAPPAPFRLLWPILGG 84
Best Local Similarity 26.1%; Pred. No. 29;
Matches 23; Conservative 11; Mismatches
                                                                                                                                                                                                                                                   85 ALSL---TFVLGLLSGFLVWRRCRRERS 109
                                                                                                                                                                                                                                                                                           | : | : | |: | |: | AYEMDTGTVRIGELAVPIICROSDRLRA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 12, 2002, 09:56:54 Job time: 111 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Accession: PC2246
A. Molecule type: mRNA
A. Residues: 1-62, RETA
A. Residues: 1-62, RETA
A. Coss-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A. Experimental source: liver
C. Genetics: 62/1
C. Superfamily: NGF receptor repeat homology
C. Reywords: transmembrane protein
C. Superfamily: signal sequence #status predicted <SIG>
F. 1-21/Domain: signal sequence #status predicted <MAT>
F. 1-21/Domain: signal sequence repeat homology <NGP>
F. 1-24/Domain: NGF receptor repeat homology <NGP>
F. 1-124/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                               C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat live
A;Reference number: JC2395; MUID:94128114
A;Accession: JC2395
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Rysmith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Yolu, D.; Spadafora, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MuID:98037514
A;Reference number: A69000; MuID:98037514
A;Reference number: A69002
A;Residues: 1-431 <ATH>
A;Residues: 1-431 <ATH>
A;Residues: 1-431 <ATH>
A;Cross-references: GB:AE000926; GB:AE000666; NID:g2622806; PIDN:AAB86156.1; PID:g262281
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487
A;Experimental source: thymus
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C;Superfamily: Methanococcus jannaschil conserved hypothetical protein MJ1681; ferredoxi
F;338-389/Domain: ferredoxin 2[4Fe-4S] homology <FER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                     C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PPAPFRLLWPILGGALSLTFVLGLLSGFLV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); DB 2; Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.3%;
Best Local Similarity 18.2%;
Matches 24; Conservative
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188 YKRYRKRQPGDP 199
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-324 <KIM>
                                                                    Fas antigen
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A.

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 12, 2002, 09:56:58 ; Search time 11.68 Seconds
 (without alignments)
 357.859 Million cell updates/sec Run on:

US-09-690-454-59 608 1 MARGSLRRLLRLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES		ID		SE	P54700			061554	SE		DROME Q24400 drosc	P53801 homo	IUMAN Q14140 homo	Q63199 rattı	IUMAN	TH 027719	P09613	Z,	063072	SE Q62424 I	P54757 ratt	Q9tv36	055058	P42514	P08563	MOUSE Q61982		008644	P23470	Q03499 hepat	095967 homo	MOUSE Q01279 mus m	_MOUSE P16283 mus m	KLK7_HUMAN P49862 homo sapien
		DB	Н					Н			Н	Н	-	Н	~1	Н	-	-	-	-	-	-	П	Н	7	Н	Н	- i	Н	Н		П	Н	
		Length	448	448	245	81	1278	2871	443	558	495	180	314	324	205	431	1008	1013	319	386	1005	2871	443	394	992	2318	245	1014	1445	123	443	1210	1227	253
ð	Query	Match	12.8				11.8	11.8	•	•	11.4	11.3	11.3	11.3	11.3	11.3	11.1	11.1	11.0	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.8	10.7	10.7	10.6	10.6	10.5	10.5	10.4
		Score	78	77	76.5	73.5	72	72	70	70	69.5	69	69	69	68.5	68.5	67.5	67.5	29	67	49	29	66.5	99	99		65.5	65	65	64.5	64.5	64	9	63.5
	Result	No.	1	7	3	4	5	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32

P17129 canis famil P71809 mycobacteri	P29319 mus musculu 002662 canis famil	083870 treponema p P56941 sus scrofa	Q05909 mus musculu P98133 bos taurus	Q03403 homo sapien P25613 saccharomyc	Q9pjp6 chlamydia m O14771 homo sapien
PSPB_CANFA	EPA3_MOUSE B3AR_CANFA	Y900_TREPA NPC1_PIG	PTPG_MOUSE FBN1_BOVIN	SP_HUMAN YCQ0_YEAST	TLC2_CHLMU 2213_HUMAN
		7		~ ~	
363	983	797	1442 2871	129	543
10.4	10.4	10.4	10.4	10.3	10.3
63.5	63.5	63	63	62.5	62.5
34	36	8 8	40	4 2 4 3	44

ALIGNMENTS

RESULT TELLS_RAT
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SUBCELLULAR LOCATION: SECRETED. SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                POTENTIAL.
                                                                                                              MGD; MGI:1346091; Fbln5.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                        InterPro; IPR001881; EGF_Ca.
Pfam; PF00008; EGF; 4.
SMART; SM00179; EGF_CA; 4.
SMART; SM0001; EGF_Like; 2.
PROSITE; PS00010; ASX_HYDROXYL; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34, Created)
34, Last sequ
36, Last anno
                                                                                                      EMBL; AF112151; AAD41767.1; -.
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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24
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247
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FLIP_SALTY
ID FLIP_SALTY
AC P54700;
DT 01-0CT-1996 (
DT 15-JUL-1998 (
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FIBULIN-5 PRECURSOR (FIBL-5) (DEVELOPMENTAL ARTERIES AND NEURAL CREST EGF-LIKE PROTEIN) (DANCE).
                                                                 (POTENTIAL).
                                              EGF-LIKE 1, DIVERGENT.

BGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                   50; Gaps
                                                                                                                                                                                                                                                                                                                                                               6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA - - PCSRGSSWSADLDXCMDCASCRARPHSDF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99357779; PubMed=10428823;
Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.;
"DANCE, a novel secreted RGD protein expressed in developing,
atherosclerotic, and balloon-injured arteries.";
J. Biol. Chem. 274:22476-22483(1999).
-1- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
LIGAND FOR INTEGRINS AND MAY PLAY A ROLE IN VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL).
: PSO1186; EGF_2; 4.
: PSO1187; EGF_CA; 6.
EGF-like domain; Calcium-binding; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                 Score 78; DB 1; Length 448;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
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                                                                                                                                                                                         SIMILARITY.
SIMILARITY.
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SIMILARITY.
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                                                                                                              BY SIMILARITY
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24.1%;
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Best Local Similarity 24.1'
Matches 26; Conservative
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                                                                                                               144
153
166
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448 AA;
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PROSITE; PS01186;
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ID FBL5_MOUSE
AC Q9WVH9;
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            PROSITE;
                                               DOMAIN
DOMAIN
                     Repeat;
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                              SIGNAL
                                                                 DOMAIN
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EGF-LIKE 1, DIVERGENT.

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00022; EGF_1; FALSE_NEG.; PS01186; EGF_2; 4.; PS01187; EGF_CA; 6. EGF-11ke domain; Calcium-binding; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
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Pred. No. 2.3;
8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CLG------AAAPPAP 74
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 AA
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71 PVKAI 75
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015118;
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NPC1_HUMAN
         RRRRAND

RRRAND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                   Schoenhals G.J., Ohnishi K., Kihara M., Macnab R.M.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A ROLE IN THE FLAGELLUM-SPECIFIC TRANSPORT SYSTEM.
-!- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MOG-2001 (Rel. 40, Last annotation update)
PYRUVATE SYNTHASE SUBUNIT PORD (EC 1.2.7.1) (PYRUVATE OXIDOREDUCTASE
PORD OR MTH1740.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LRRLLRLLVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRRLLFLSLAGLW--LFSPAAAAQLPGLISQPLAGGGQSWSLSVQTLVFITSLTFLPAIL 58
                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 --HSDF-------CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
C9A4241F0653A4D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76.5;
Pred. No. 1.
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FLAGELLAR BIOSYNTHETIC PROTEIN FLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0951; FIGBIOSNFLIP.
ProDom; PD002586; Flip; 1.
PROSTTE; PS01060; FLIP_1; 1.
PROSTTE; PS01061; FLIP_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26787 MW;
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30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          StyGene; SG10577; flip.
InterPro; IPR002039; Flip.
Pfam; PF00813; Flip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flagella; Transmembrane.
TRANSMEM 4 24
TRANSMEM 45 65
                                                             Salmonella typhimurium
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185
209
245 AA;
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                       NCBI_TaxID=602;
                              FLIP OR FLAR
                                                                                                                           Salmonella.
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TRANSMEM
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Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

-! CATALTIC ACTIVITY: PYRUYATE + COA + OXIDIZED FERREDOXIN = ACETYL-COA + CO(2) + REDUCED FERREDOXIN.
-! COFACTOR: BINDS TWO 4FE-4S CLUSTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
-!- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PGTAPCSRGSSWSA----DLDKCMDCASCRA-----RPHS---DFCLGCA-AAPPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 PGSTVKNKTGSWRTFKPVLDKDKCIDCDNCILFCPEGCINREHEIDYDYCKGCGICAEKC 70
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON-SULEUR 1 (4FE-4S) (POTENTIAL).
IRON-SULEUR 1 (4FE-4S) (POTENTIAL).
IRON-SULEUR 1 (4FE-4S) (POTENTIAL).
IRON-SULEUR 2 (4FE-4S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0353; 4FE4SFRDOXIN.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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MEDLINE-97362323; PubMed-9211849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000929; AAB86210.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO0151, 4FE4S_ferrdxin. Pfam; PF00037; fer4; 2. PRINTS; PR00353; 4FE4SFRDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIEMANN-PICK C1 PROTEIN PRECURSOR.
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9121 MW;
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Best Local Similarity 29.2
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      GAMMA CHAIN.
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Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A., Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T., "Niemann-Pick Cl disease: the 11061T substitution is a frequent mutant allele in patients of Western European descent and correlates with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
MEDLINE=99408226; PubWed=10480349;
Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
Akaboshi S., Watanabe Y., Takeshina T., Inui K., Okada S., Tanaka A.,
Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTIONAL INTEGRITY OF NERVE TERMINALS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE
ENDOSOMES AND IXSOSOMES.
DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN
CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYSOSOMAL TARGETING
ARE CRITICAL FOR MOBILIZATION OF CHOLESTEROL FROM LYSOSOMES.
PTM: GLYCOSYLATED.
DISEASE: DEFECTS IN NPC1 ARE THE CAUSE OF NIEMANN-PICK TYPE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S., Newfeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III; "Niemann-Pick CI protein: obligatory roles for N-terminal domains and lysosomal targeting in cholesterol mobilization."; Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D., Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B., Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A., Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R., Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y., Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J., Markle D., O'Neill R.R., van Diggelen O.P., Elleder M., Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.; "Niemann-Pick Cl disease gene: homology to mediators of cholesterol homeostasis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS NPC1 Q-934; L-940; N-948; L-954; W-992; A-1007; T-1061 AND V-1213,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98299797; PubMed-9634529; Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M., Byers D.M., Dobson M.J., Neumann P.E.; "The Nova Scotia (type D) form of Niemann-Pick disease is caused by G3097-->T transversion in NPCL";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'NPC1 gene mutations in Japanese patients with Niemann-Pick disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. 105:10-16(1999).
FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF CHOLESTEROL. MAY PLAY A ROLE IN VESICULAR TRAFFICKING IN GLIA, PROCESS THAT MAY BE CRUCIAL FOR MAINTAINING THE STRUCTURAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C., Neumann P.E.;
                                                                                                                                                                                                                                                                                                                                                           "The genomic organization and polymorphism analysis of the human Niemann-Pick Cl gene."; Biochem. Biophys. Res. Commun. 261:493-498(1999).
                                                                                                                                                                                                                                                                                                                 Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
Carstea E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           classic juvenile phenotype.";
Am. J. Hum. Genet. 65:1321-1329(1999).
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANTS.
MEDLINE-99355599; Pubmed-10425213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99128318; Pubmed=9927649;
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                                                                                                                                                                                                                            Science 277:228-231(1997).
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DISEASE, AN AUTOSOMAL RECESSIVE LIPID STORAGE DISORDER WHICH AFFECTS PARTICULARLY THE BRAIN, LIVER AND SPLEEN AND WHICH IS CHARACTERIZED BY PROGRESSIVE NEUROBEGENERATION AND VARIABLE HEPATOSPLENOMEGALY. THE DISEASE IS DIVIDED INTO TYPE C (NPC OR NPCI) AND THE LESS SEVERE TYPE D (NPD), ALSO KNOWN AS NOVA SCOTIA TYPE. IT IS CHARACTERIZED BY LYSOSOMAL ACCUMULATION OF LOW DENSITY LIPORROTEIN DERLYED CHOLESTENGL. CLINICAL FEATURES INCLUDE CAN VARY FROM INFANCY TO LATE ADULTHOOD.
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POLY-PRO.
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InterPro; IPR003392; Patched.
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EMBL; AF157372;
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Biol. Chem. 270:1798-1806(1995).
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                     SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Kidney;
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HSSP;
7;
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                                                                                                                                                                                                               /FTId=vAR_008830.
S -> L (IN NPC1).
/FTId=vAR_008831.
C -> Y (IN NPC1; LATE INFANTILE FORM).
/FTId=vAR_008832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95130561; PubMed=7829516;
Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,
Pereira L., Ramirez F., Bonadio J.;
"Primary structure and developmental expression of Fbn-1, the mouse
S (IN NPC1; LATE INFANTILE FORM).
                                  /FTIG=VAR_008819.

S -> P (IN NPC1; LATE INFANTILE FORM).
/FTIG=VAR_008820.
H -> P (IN NPC1; LATE INFANTILE FORM).
/FTIG=VAR_008821.
R -> Q (IN NPC1; LATE INFANTILE FORM).
COMMON IN JAPANESE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FBN1 OR FBN-1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                         I -> V (FREQUENT POLYMORPHISM IN JAPANESE).
                                                                                                                                                                                                                                                                                                     DB 1; Length 1278;
                                                                                                                                      /FTIG=VAR_000825.
V -> M (IN NPC1; ADULT FORM).
/FTIG=VAR_008826.
Q -> P (IN NPC1).
/FTIG=VAR_008827.
                                                                                                                                                                                                                                                                                                                    17; Indels
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P -> A (IN NPC1).
/FTId=VAR_008834.
                                                                                                                                                                                  /FTId=VAR_008828.
S -> L (IN NPC1).
/FTId=VAR_008829.
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      FTId=VAR_008817
                     /FTId=VAR_008818
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V -> A.
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                                                                                                                                                                             R -> Q (IN NPC1)
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8; Mismatches
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273 WITYMAFLLVFFGAFFAVW--CYRKR 296.
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                                                                                                                                                                                                                                                                                                     11.8%;
31.4%;
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Best Local Similarity 31.4
Matches 27; Conservative
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R InterPro; IPR000152; Asx_hydroxyl.

R InterPro; IPR001521; EgF-like.

R InterPro; IPR001881; EGF-Ca.

R InterPro; IPR002212; TB.

R Ffam; PF00008; EGF; 46.

R Ffam; PF00009; EGF; 46.

R SMART; SM00019; EGF_CA; 42.

R SMART; SM00010; ASX_HYDROXIL; 43.

R ROSITE; PS001001 ASX_HYDROXIL; 43.

R ROSITE; PS01186; EGF_21; 2.

R ROSITE; PS01186; EGF_21; 38.

R ROSITE; PS01187; EGF_CA; 45.

R ROSITE; PS01187; EGF_CA; 45.

R ROSITE; PS01187; EGF_CA; 45.
                                                                                                                                                                                                                                MICROFIBRILS (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING
Ota K., Kumar A., Wada J., Liu 2., Kanwar Y.S.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
- THAT BINDS CALCIUM: FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
                                                                                                                                                             -!- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING.
BINDING.
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                                                                                                                                                                                                                                                                                               EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.

EGF-LIKE 6, NON-CALCIUM BINDING
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 9, CALCIUM-BINDING.
EGF-LIKE 10, CALCIUM-BINDING.
EGF-LIKE 11, CALCIUM-BINDING.
EGF-LIKE 12, CALCIUM-BINDING.
EGF-LIKE 13, CALCIUM-BINDING.
EGF-LIKE 14, CALCIUM-BINDING.
EGF-LIKE 15, CALCIUM-BINDING.
EGF-LIKE 16, CALCIUM-BINDING.
EGF-LIKE 17, CALCIUM-BINDING.
EGF-LIKE 17, CALCIUM-BINDING.
EGF-LIKE 17, CALCIUM-BINDING.
EGF-LIKE 18, CALCIUM-BINDING.
EGF-LIKE 21, CALCIUM-BINDING.
EGF-LIKE 21, CALCIUM-BINDING.
EGF-LIKE 21, CALCIUM-BINDING.
EGF-LIKE 22, CALCIUM-BINDING.
EGF-LIKE 23, CALCIUM-BINDING.
EGF-LIKE 24, CALCIUM-BINDING.
EGF-LIKE 24, CALCIUM-BINDING.
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NON-CALCIUM BINDI
CALCIUM-BINDING.
CALCIUM-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Signal; Multigene family.
SIGNAL 1 27 POTENTIAL.
CHAIN 28 2871 FIBRILLIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE 3, 1
EGF-LIKE 4, C
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EGF-LIKE 2,
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DISULFID 1081	DISULFID 1117	FT DISULFID 1124 1138 FT DISULFID 1140 1153	DISULFID 1159	DISULFID 1182	DISULFID 1201	DISULFID 1223	1242	DISULFID 1249	DISHLEID 1283	DISULFID 1291	DISULFID 1307	DISULFID 1326	DISULFID 1333	DISULFID 1350	DISULFID 130/	DISCHIETD 1301	DISCHE TO 1991	DISHLFID 1415	DISULFID 1431	DISULFID 1450	DISULFID 1456	DISULFID 1472	DISULFID 1491	1497	DISULFID 1610	DISULFID 1617	DISULFID 1633	DISULFID 1652	DISULFID 1658	ם ונ	Query March	20; Conservative		Qy 36 CSRGSSWSADLDKCMD	: :	0 * 0 7	Qy 68 AAAPPAPFRLLWPILGGAL 86	:: - -: = -	DD 2100 PTEPDEAFRQICPFGSGII 2118		RESULT 7	FBL4_MOUSE	ID FBL4_MOUSE STANDARD;	AC QSWV33; DT 20-AHG-2001 (Rel 40, Created)	2001 (Rel. 40	DT 20-AUG-2001 (Rel. 40, Last and	DE EGF-CONTAINING FIBULIN-LIKE E)	DE (FIBULIN-4) (FIBL-4) (MUTANT I	GN EFEMPZ OR FBLN4 OR MBPL.	cuius (mouse). ta; Metazoa: Chordata	OC Mammalia; Eutheria; Rodentia;	xID=10090;	RN [1]	RE SEQUENCE FROM N.A. RC STRAIN=C57B1,/6.T:	=99308589; PubMed=1	RA Gallagher W.M., Argentini M.,	ier E.; a novel mutant n53-	500
EGF-LIKE 25, CALCIUM-BINDING, EGF-LIKE 26, CALCIUM-BINDING		EGF-LIKE 28, CALCIUM-BINDING. EGF-LIKE 28, CALCIUM-BINDING.	6	EGF-LIKE 30, CALCIUM-BINDING.	32,	33,	34,	,00	36.	37,	38,	EGF-LIKE 39, CALCIUM-BINDING.	40,	-	EGETLIKE AS CALCIUM-BINDING.	7 7	` <	45,	46,	47,	RIT	BY SIMILARITY.	BI SIMILARIII.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	KLTY.	RITY.	RITY.	RITY.	KIIX.	RITY.	RITY.	RITY.	RITY.	KLTY.	RITI.	RITY.	RITY.	RITY.	RITY.	RITY.	RITY.	RITY.		RITY							
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1446	1528	1648	1689	1808	1847	1930	1973	2055	2127	2166	2206	2247	2291	2333	2402	2485	2524	2567	2607	2648	82	8 6	102	123	136	150	154	168	250	273	292	299	315	453	400	494	499	515	54.4 7.4.1	557	216	282	576	623	639	727	734	06/	776	792	811	816	932	921	937	1032	1055	1074
FT DOMAIN													٠																																													
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	DISULFID DIS	FT DISCULLID 1658 1672 Ouery Match Best Local Similarity 25.3%; Matches 20; Conservative 7 Oy 36 CSRGSSWSADLDKCMD Db 2040 CPEGFSWSSGGRRCODLRMSYCYA OY 68 AAAPPAPFRILWPILGGAL 86

us-09-690-454-59.rsp

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558 AA.
                     62 ----- DFCLGCAAA------ PPAP 74
                                          72 INHYGGYLCLPRSAAVISDLHGEGPPPP 99
                                                                                                  PRT;
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515
558 AA;
                                                                                                                                                                                         NCBI_TaxID=10116;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                      SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEF-LIKE 1, DIREGENT.

EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LLIWAFILLILGAASPODPEEPDSYTECTDGYEWDADSQHCRDVNECLTIPEACKGEMKC 71
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N-LINKED (GLCNAC. .) (POTENTIAL).
4969C0328A23DD88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wery match
Best Local Similarity 27.3%; Pred. No. 10;
Matches 24; Conservative 5; Mismatches 33. Tables
                     SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATRIX PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 4.

PRINTS; PR00907; THRMBOMODULN.
SMART; SM00179; EGF_CA; 4.

SMART; SM00179; EGF_L1ke; 2.

PROSITE; PS00010; ASX HYDROXYL; 4.

PROSITE; PS01186; EGF_1; FALSE_NEG.

PROSITE; PS01187; EGF_C3; 6.
                                                                                                                                                                                                                                                                                       MGD; MGI:1891209; Efemp2.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001491; Thimbomoduln.
                                                                                                                                                                                                                                                                      EMBL; AF104223; AAD45219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49425 MW;
Oncogene 18:3608-3616(1999)
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SEQUENCE
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N-LINKED (GLCNAC. ...) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
T -> A (IN REF. 2).
T -> A (IN REF. 2).
A -> G (IN REF. 2).
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A -> D (IN REF. 2).
B -> D (IN REF. 2).
C -> D (IN REF. 2).
A -> G (IN REF. 2).
                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAY PLAY AN IMPORTANT ROLE IN THE TROPHIC AND INJURY RESPONSES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
-!- PTM: THIS CELL-ASSOCIATED GLYPICAN IS FURTHER PROCESSED TO GIVE
RISE TO A MEDIUM-RELEASED SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02896; AAA86439.1; -.
EMBL; L34067; AAA41251.1; -.
PIR; JG1281; JG21281.
InterPro; IPR001863; Glypican.
Pfam; PF01153; Glypican; 1.
PROSITE; PS01207; GLYPICAN; 1.
Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED IN MATURE FORM (POTENTIAL). GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93038690; PubMed-1417860; Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis "Cloning of a major heparan sulfate proteoglycan from brain an identification as the rat form of glypican."; Biochem. Biophys. Res. Commun. 188:395-401(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE GLYPICAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 1;
Pred. No. 13;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-04UG-2001 (Rel. 40, Last annotation update)
GLYPICAN-1 PRECURSOR (HSPG M12).
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Best Local Similarity
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170 KGCYAKKFGPKGYGYGQGGGAL 191
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Hendelarson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Berraz C., Ferriera S., Fleischmann W.,
RA Chodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Godek A., Gong Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.L., Harvey D., Heiman T.J., Herris W., Glasser K.,
RA Harris N.L., Houston K.A., Howland T.J., Well M. H., Ibegwam C.,
Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Howland T.J., Heiman T.J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harris N.L., Moy M., Moy W., Woberry C., Morlis J., Puckers M.G.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Puckers M.G.,
RA Reinert K., Remington K., Sampson M., Stupski M.P., Smith T.,
RA Beiter E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Shie B.C., Siden K.A., Massarman D.A., Weissenbach J.,
RA Stirskas R., Tector C. Turner E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 5,
                                                                                                                                                                                                                                                                                                                                                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
1; Drosophilidae; Drosophila.
                                                 11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;
"Muscle LIM proteins associate with muscle sarcomeres and require
dMEP2 for their expression during Drosophila myogenesis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 18;
                                                                                                                                                                                                                                                                                                LIM3 OR MLP84B OR CG10699.
Drosophila melanogaster (Fruit fly).
Elvaryota; Matazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyeera; Musc
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96387325; PubMed-8794860;
Stronach B.E., Siegrist S.E., Beckerle M.C.;
"Two muscle-specific LIM proteins in Drosophila.";
J. Cell Biol. 134:1179-1195(1996).
19;
                                                                                                                                                                                       DROME SIGNES SIGNES OF A PAGE 1970 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 1-NOV-1997 (Rel. 40, Last annotation update) 1-NOV-1997 (Rel. 40, Last annotation update) 1-NOV-1997 (Rel. 40, Last annotation update)
 Mismatches
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MEDLINE-20196006; PubMed-10731132;
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26; Conservative
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                                                                                                                           273 RNVLKGCLA 281
                                                                                          65 ---- LGCAA 69
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MLP2_DROME
Matches
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                                                                                                                                                                             - FUNCTION: PLAYS A ROLE IN CELL DIFFERENTIATION LATE IN MYOGENESIS.
- SUBCELLULAR LOCATION: UNCLEAR, AND CYTOPLASMIC.
- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSION IS RESTRICTED TO THE SOMATIC, VICERAL, AND PHARYMEAL MUSCLES. WITHIN THE SOMATIC MUSCULATURE, MICHAED IS LOCALIZED AT THE ENDS OF MUSCLES FIBERS AT THE POINT OF ATTACHMENT TO THE PEIDERMIS. THERE IS NO EXPRESSION IN CARDIAC MESODERM OF IN FAT BODY.
- DEVELOPMENTAL STAGE: EXPRESSION IS BIPHASIC, PEAKING LATE IN EMBRYOGENESIS (16-24 HEMBRYOS) AND DOBING THE LAND YOUND IN DEVELOPING MUSCLES OF THE VISCERAL AND SOMATIC MESODERM SUBSEQUENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00478; LIM_DOMAIN_1; 5.
PROSITE; PS500478; LIM_DOMAIN_2; 5.
Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis;
Developmental protein; Differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AIARAPEGEGCPRCGGYVYAAEQMLARGRSWHKECFKCGTCKKGLDSILCCEAPDKNIYC 169
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO THE FORMATION OF THE MUSCLE PRECURSOR CELLS. DECREASED LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARE STILL DETECTABLE IN ADULTS.
SIMILARITY: TO THE VERTEBRATE CYSTEINE-RICH PROTEINS.
SIMILARITY: CONTAINS 5 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLRSVAGEQAP-----CTAPCSRGSSWSADLDKCMDCAS------CRARPHSDFC
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                                                                                          Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
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LIM 3.
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LIM 4.
GLY-RICH.
LIM 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF090832; AAC61591.1; -. EMBL, AE003672; AAF54063.1; -. HSSP; Q05158; 1QLI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0014863; Mlp84B.
Interpro; IPR001781; LIM.
Pfam; PF00412; LIM; 5.
ProDom; PD000094; LIM; 5.
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28.0%;
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CONFLICT
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MEDLINE-20289799; PubMed-10830953;

MEDLINE-20289799; PubMed-10830953;

MEDLINE-20289799; PubMed-10830953;

MEDLINE-20289799; PubMed-10830953;

MEDLINE-20289799; PubMed-10830953;

AND ARK H.-S., Toyoda A., Tshili K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Amerason D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shimtani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Schoen O., Desario A., Rakchelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Lehrach H., Reinhardt R., Yaspo M.-L., Lehrach H., Reinhardt R., Yaspo M.-L., Lehrach H., Reinhardt R., Yaspo M.-L., The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             "Cloning of a novel human putative type Ia integral membrane protein mapping to 21922.3.";
Genomics 49:133-136(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SUBCELLULAR LOCATION: ACCORDING TO REF.3, IT IS FOUND IN THE CYTOPLASM AND IN THE NUCLEUS. ACCORDING TO REF.1, IT IS A TYPE I MEMBRANE PROTEIN.
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PIPYWRLRLGG -> ARRIGGCASV (IN REF. 3).
          PTTG_HUMAN STANDARD; PRT; 180 AA.
901-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-NUG-2001 (Rel. 40, Last annotation update)
20-NUG-2001 (Rel. 40, Last annotation update)
PTUTTARY TUMOR-TRANSFORMING GENE 1 PROTEIN INTERACTING PROTEIN
BINDING FACTOR) (PBF)
                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yaspo M.-L., Aaltonen J., Horelli-Kuitunen N., Peltonen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE=20317150; Pubmed=10781616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                TISSUE-1117mus,
MEDLINE-98234553; PubMed-9570958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003659; PSI.
SMART; SM00423; PSI; 1.
Transmembrane; Nuclear protein.
TRANSMEM 97 117 PO
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                                                                                                                    PITGIIP OR C210RF1 OR C210RF3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 405:311-319(2000).
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                   Lehrach H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                               67 CAAAPPAP----FRLLW-----PILGGALSLTFVLGLLSGFLVWRRCRRER 108
                                                                                                                                                                                                                                                                                                                                                                                                      72 TSVLPPASLCKLSSARWGVCWVNFEALIITMSVVGG----TLLLGI--AICCCCCRRKR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                  10 LRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLG--- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.; "Prediction of the coding sequences of unidentified human genes. IV. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by analysis of cDNA clones from human cell line KG-I."; DNA Res. 2:167-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
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114 TLLLGIA -> NPPPGHC (IN REF. 3).
20323 MW; F1E66014D49EC1DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%; Score 69; DB 1; Length 314; 34.0%; Pred. No. 9.7; tive 6; Mismatches 27; Indels
                                                                                                                  DB 1; Length 180;
                                                                                                                                                                       19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AA; 33896 MW; E43107FC565AAC31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN KIAA0127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASA_RAT STANDARD; PRT; 324 AA. 063199; 15-JUL-1999 (Rel. 38, Created) 20-AUG-1999 (Rel. 38, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                            Ouery Match
11.3%; Score 69; DB 1
Best Local Similarity 25.8%; Pred. No. 6.1;
Matches 32; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
MEDLINE=96127530; PubMed=8590280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D50917; BAA09476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 34.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 SSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 SRKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y127_HUMAN
Q14140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA0127
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---PPAPFRLLWPILGGALSLTFVLGLLSGFLV 100

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61 -SDFCLGCAAA---
                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  like (GSCL) ho
development.";
                                                                                                                                                                     30-MAY-2000
30-MAY-2000
                                                                                                                                                          30-MAY-2000
                                                                                                                                     GSCL_HUMAN
                                                                                                                                               015499
                                                                                                                        GSCL_HUMAN
                                                                                                                                                                                                            GSCL.
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                                               Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                 BIOCHEM. BIOPHYS. RES. COMMUN. 198:666-674(1994).

-I-FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADARTOR WOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULFING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERRORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INTITATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUTCIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 APGTAPCSRGSSWSAD---LDKCMDCA----------SCRARPH----- 60
                                                                                                                                 Kimura K., Yamamoto M., Wakatsuki T.;
"A variant mRNA species encoding a truncated form of Fas antigen in
                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0652; TNFR_NGFR_1; 2.
PROSITE; PSO0652; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal. SIGNAL 22 324 FASL RECEPTOR.
PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.3%; Score 69; DB 1; Length 324; 18.2%; Pred. No. 10; tive 18; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D25D583C909D9D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). 3 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                       MEDLINE=94128114; PubMed=7507668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D26112; BAA05108.1; -.
InterPro: IPR000488; Death.
InterPro: IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR, 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
188
324
163
79
123
303
            (APO-1 ANTIGEN) (CD95
INFRSF6 OR PT1 OR FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                               SEQUENCE FROM N.A.
 RECEPTOR
                                                                                                                                                       the rat liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Am. J. Hum. Genet. 60:1194-1201(1997).

-!- FUNCTION: MAY HAVE A ROLE IN DEVELOPMENT. MAY REGULATE ITS OWN
TRANSCRIPTION. MAY BIND THE BICOID CONSENSUS SEQUENCE TAATCC.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- TISSUE SPECIFICITY: DETECTED IN ADULT TESTIS AND PITUITARY, AND IN
9-10 WK FETAL TISSUE (THORAX). PROBABLY EXPRESSED IN OTHER TISSUES
AT LOW LEVELS.

-!- DEVELOPMENTAL STAGE: EXPRESSED IN EARLY HUMAN DEVELOPMENT AS WELL
    ---FI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DiGeorge syndrome minimal critical region contains a goosecoid-
like (GSCL) homeobox gene that is expressed early in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT CYS-47.

MEDLINE=98110571; PubMed=9441739;
Funke B., 5 Jore B., Puech A., Sirotkin H., Edelmann L., Carlson C.
Funke B., 7 Jore B., Pucherlapati R., Skoultchi A., Morrow B.E.;
"Characterization and mutathon analysis of goosecoid-like (GSCL), a homeodomain-containing gene that maps to the critical region for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VCFS/DGS). SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AS IN A LIMITED NUMBER OF ADULT TISSUES.
DISEASE: MAY BE RELATED TO SOME OF THE DEVELOPMENTAL DEFECTS
ASSOCIATED WITH VELOCARDIOFACIAL AND DIGEORGE SYNDROMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97294411; PubMed-9150167;
GOTLINE-9729418. Emanuel B.S., Driscoll D.A., Sellinger B., Wang Z.,
Roe B., Budarf M.L.;
135 LCDHCYHCTSCGLEDILEPCTRTSNTKCKKQSSNYKLLWLLILPGLAILFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEDBOX_1; 1.
PROSITE; PS50071; HOMEDBOX_2; 1.
HOMEOBOX; DNA-binding; Nuclear protein; Polymorphism.
5 POLY-ALA.
DOMAIN 64 70 POLY-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               205 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX PROTEIN GOOSECOID-LIKE (GSC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P06601; 1FJL.
MIM; 601845; -.
InterPro; 1FR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U96402; AAC39544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCFS/DGS on 22q11.";
Genomics 46:364-372(1997).
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "BICOID" SUBFAMILY
                                                                                       101 WRRCRRERSSPP 112
                                                                                                                                                              188 YKKYKKROPGDP 199
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82
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-98037514; pubMed-9371463; Smith D.R., Deucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wlerzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol., 179:7135-7155 (1997).
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                       26 AGEQ------APGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFR 76
                                                                                                                                               45 AGROSPAKPEEPGAPEAAPCA-------CCCCCGPRAAP----CGPPEAAGLGAR 89
                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                 33;
                                                                         Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 431;
                                                                                                31; Indels
       R -> C.
/FTId=VAR_008549.
: 665C33D9C454E7A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 431 AA: 46950 MW; 802FA39757194B85 CRC64;
                                                                                                                                                                      27;
                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: STRONG, TO M. JANNASCHII MJ1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD011569; DUF39; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                    (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                      Score 68.5; DE Pred. No. 7.6; 6; Mismatches
                                                                                                                                                                                                                                                               431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 68.5; Di
26.1%; Pred. No. 14;
tive 11; Mismatches
 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001450; 4FE4S_ferrdxin.
InterPro; IPR002708; DUF39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000926; AAB86156.1; -.
                                  21545 MW;
                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN MTH1684.
                                                                      11.3%;
ilarity 31.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01837; DUF39; 1
Pfam; PF00037; fer4; 2.
                                                                                                                                                                                                                                                                                                                                                                           Methanothermobacter.
                                 205 AA;
                                                                                   Best_Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00198; 1FDN
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DELTA H:
                                                                                                                                                                                                                                                                                     15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                            YG84_METTH
O27719;
                                                                                                                                                                                                                                                                                                               20-AUG-2001
DNA_BIND
VARIANT
                                   SEQUENCE
                                                                         Query Match
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FTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete nucleotide sequence of the M RNA segment of Uukuniemi virus encoding the membrane glycoproteins Gl and G2."; Virology 160:191-202(1987).
-!- PTM: SPECIFIC ENZYMATE CLEAVAGES IN VIVO YIELD MATURE PROTEINS INCLUDING NONSTRUCTURAL PROTEIN NS-M, GLYCOPROTEIN G1, AND
1-NOV-1995 (Rel. 32, Last sequence update)
0-AUG-2001 (Rel. 40, Last annotation update)
POLYPROTEIN PRECURSOR [CONTAINS: GLYCOPROTEIN G1; GLYCOPROTEIN G2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 APGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPF-----RLLWPI 81
                                                                                                                                                                                                                                                                                                                                                                  negative-strand viruses; Bunyaviridae; Phlebovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTI)
MW; F557C06D8DB77E32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 OF 18-29 AND 514-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Signal.
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POTENTIAL
N-LINKED (GLCNAC
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                                                                                                                                                                                                   1008 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 67.5; 23.6%; Pred. No. 36;
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                                                          85 ALSL---TFVLGLLSGFLVWRRCRRERS 109
                                                                                                385 AYEMDTGTVRIGELAVPIICROSDRLRA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE (MEDLINE=87321102; Pubmed=3629974;
                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M17417; AAA79512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ronnholm R., Pettersson R.F.
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Polyprotein; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 23.6
Matches 21; Conservative
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1008
415
1003
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208
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691
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                                                                                                                                                                                                                                                                                                                                                  Uukuniemi virus (Uuk)
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11591;
                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA
                                                                                                                                                                                                                                                                                       20-AUG-2001
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SEQUENCE
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CHAIN
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42 WSADL-----DKCMDCASC----RARPHS-----DFCLGCAAAPPAPFRLLWPILGG 84

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Search completed: March 12, 2002, 10:00:06 Job time: 188 sec

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